

103	32	51.6	307	2	T34143
104	32	51.6	311	2	AB3154
105	32	51.6	323	2	PT5202
106	32	51.6	325	2	S55306
107	32	51.6	326	2	A99133
108	32	51.6	327	2	S8305
109	32	51.6	344	2	A72780
110	32	51.6	354	2	T36649
111	32	51.6	361	2	H36943
112	32	51.6	366	1	A0056
113	32	51.6	366	1	JC1106
114	32	51.6	368	2	D93823
115	32	51.6	380	2	AG2148
116	32	51.6	383	2	HB4156
117	32	51.6	386	2	T9256
118	32	51.6	388	2	S76932
119	32	51.6	397	2	B66663
120	32	51.6	402	2	S55980
121	32	51.6	432	2	AC2146
122	32	51.6	436	2	AC1021
123	32	51.6	437	2	C91261
124	32	51.6	437	2	G6101
125	32	51.6	437	2	T39566
126	32	51.6	452	2	S18451
127	32	51.6	476	2	D95221
128	32	51.6	480	2	C8085
129	32	51.6	480	2	A27626
130	32	51.6	481	2	A0761
131	32	51.6	487	1	BNSGM
132	32	51.6	524	2	D70861
133	32	51.6	531	2	T30167
134	32	51.6	552	2	E75322
135	32	51.6	554	2	T83790
136	32	51.6	567	1	A0FFA1
137	32	51.6	567	2	H34445
138	32	51.6	573	2	S71210
139	32	51.6	583	2	T1210
140	32	51.6	588	2	T45339
141	32	51.6	593	2	AP1011
142	32	51.6	605	2	T25282
143	32	51.6	640	1	VCVWM1
144	32	51.6	665	1	VCVWEM
145	32	51.6	693	2	G81725
146	32	51.6	699	2	AB3375
147	32	51.6	711	1	TPFL
148	32	51.6	736	2	S23654
149	32	51.6	754	2	D70536
150	32	51.6	775	2	T30917
RESULT 1					
C2231					
C:Superfamily: prostacyclin synthase/cholesterol 7alpha-monoxygenase (cytochrome P450 CYP)					
C:Keywords: intramolecular oxidoreductase; isomerase					
C:Accession: JG2231; MUID:94242046; PMID:8105632					
C:Reference number: JG2231; MUID:94242046; PMID:8105632					
C:Residues: 1-1500 <M1Y>					
C:Cross-references: UNIPROT:Q16647; GB:D98145; NID:9537948; PIDN:BAA07343.1; PID:9537949					
C:Experimental source: aortic endothelial cell					
C:Comment: This enzyme catalyzes the conversion of prostaglandin H2 to prostaglandin I2.					
C:Accession: JC2231 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004					
C:Title: Molecular cloning and expression of human prostacyclin synthase.					
C:Author: Miya, A.; Yokoyama, C.; Inoue, H.; Ulrich, V.; Tanabe, T.					
C:Journal: Biophys. Res. Commun. 200, 1728-1734, 1994					
C:Year: 1994					
C:Page: 1728-1734					
C:PMID: 8105632					
C:Map position: 20q13.11-q13.13					
C:Accession: A99133					
C:Title: Isolation and molecular cloning of prostacyclin synthase from bovine endothelial cell					
C:Author: Hara, S.; Miyata, A.; Yokoyama, C.; Inoue, H.; Brugger, R.; Lottspeich, F.; Ullrich, V.					
C:Journal: J. Biol. Chem. 269, 19897-19903, 1994					
C:Year: 1994					
C:Page: 19897-19903					
C:PMID: 8074709					
C:Accession: A53658					
C:Title: mRNA					
C:Accession: A53558					
C:Title: prostaglandin-I synthase (EC 5.3.99.4) - bovine					
C:Accession: A53558; JG2231; PC227; PC2016					
C:Title: prostacyclin synthase (EC 5.3.99.4) - bovine					
C:Accession: A53558; JG2230; MUID:94354863; PMID:8074709					
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C:Title: prostacyclin synthase					
C:Accession: A53558; JG2230; MUID:94354863; PMID:8074709					
C:Title: prostacyclin synthase					
C:Accession: A53558; JG2230; MUID:94354863; PMID:8074709					
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C:Accession: A53558; JG2230; MUID:94354863; PMID:8074709					
C:Title: prostacyclin synthase					
C:Accession: A53558; JG2230; MUID:94354863; PMID:8074709					
C:Title: prostacyclin synthase					
C:Accession: A53558; JG2230; MUID:94354863; PMID:8074709					
C:Title: prostacyclin synthase					
C:Accession: A53558; JG2230; MUID:94354863; PMID:8074709					

A;Accession: T04523
A;Molecule type: DNA
A;Residues: 1-880 <BEV>
A;Cross-references: UNIPROT:Q9SVU3; EMBL:AL035353
A;Experimental source: cultivar Columbia; BAC clone F16A16
C;Genetics:
A;Map position: 4
A;Introns: 6/0/1
A;Note: F16A16.130

Query Match 64.5%; Score 40; DB 2; Length 880;
Best Local Similarity 60.0%; Pred. No. 25; Mismatches 1; Indels 0; Gaps 0;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GIEALPRTHE 10
Db 44 GIEALPQHQ 53

RESULT 4
D85727 oxygen sensing protein [similarity] - Escherichia coli (strain 0157:H7, substrain EDL933 C;Species: Escherichia coli
C;Accession: D85727
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 16-Aug-2004
R;Perse, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamitis, K.; Apodaca, Nature 409, 529-533, 2001.
A;Title: Genome sequence of enterohemorrhagic Escherichia coli 0157:H7.
A;Reference number: A85480; MUID:2107935; PMID:11208551
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-367 <STO>
A;Experimental source: strain 0157:H7, substrain EDL933
C;Genetics:
A;Gene: 2221
C;Superfamily: Oxygen sensor diguanylate cyclase/c-di-GMP phosphodiesterase

Query Match 62.9%; Score 39; DB 2; Length 367;
Best Local Similarity 66.7%; Pred. No. 15; Mismatches 3; Indels 0; Gaps 0;
Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GIEALPRTHESQ 12
Db 142 GIEALARMHQ 153

RESULT 5
E90890 oxygen sensing protein [imported] - Escherichia coli (strain 0157:H7, substrain RIMD 050 C;Species: Escherichia coli
C;Accession: E90890
C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 16-Aug-2004
R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.; Gabawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H. DNA Res. 8, 11-22, 2001.
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli 0157:H7 and gene A;Reference number: A99629; MUID:21156231; PMID:11258796
A;Accession: E90890
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-367 <HAY>
A;Experimental source: strain RIMD 050952
A;Residues: 1-367 <HAY>
A;Cross-references: UNIPROT:Q8XAUB; GB:BA00007; PIDN:BAB35516.1; PID:gi3361559; GSPDB:Q A;Experimental source: strain 0157:H7, substrain RIMD 050952
C;Genes: Ecs2033
C;Genetics:
A;Gene: Ecs2033
C;Superfamily: Oxygen sensor diguanylate cyclase/c-di-GMP phosphodiesterase

Query Match 62.9%; Score 39; DB 2; Length 367;
Best Local Similarity 66.7%; Pred. No. 15; Mismatches 3; Indels 0; Gaps 0;

RESULT 6
JCT7363 95K retinoblastoma protein-binding protein - human
C;Species: Homo Sapiens (man)
C;Accession: 17-Nov-2000 #sequence_revision 17-Nov-2000 #text_change 09-Jul-2004
R;Men, H.; Ao, S.; Biochem. Biophys. Res. Commun. 275, 141-148, 2000
A;Title: RB95, a novel leucine zipper protein, binds to the retinoblastoma protein.
A;Reference number: JCT7363
A;Contents: Petal brain
A;Accession: JCT7363
A;Molecule type: mRNA
A;Residues: 1-838 <WEN>
A;Cross-references: UNIPROT:Q9HC82; GB:AF122819
C;Comment: This protein, a member of retinoblastoma protein-associated protein and a leucine zipper, mediates transcription and/or transcriptional processing.

C;Genetics:
A;Gene: rbp95
A;Map position: 16p11.2-16p11.1
A;Keywords: leucine zipper; transcription regulation.

Query Match 62.9%; Score 39; DB 2; Length 838;
Best Local Similarity 72.7%; Pred. No. 36; Mismatches 8; Conservative 7; Mismatches 2; Indels 0; Gaps 0;

Qy 2 IEALPRTHESQ 12
Db 105 VEALLRCHBSQ 115

RESULT 7
B75634 hypothetical protein - Deinococcus radiodurans (strain R1)
C;Species: Deinococcus radiodurans
C;Accession: B75634
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma, S.; Shen, M.; Vaishnavan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.M. Science 286, 1571-1577, 1999.
A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A;Reference number: A75250; MUID:20036896; PMID:10567266
A;Accession: B75634
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-442 <WHT>
A;Cross-references: UNIPROT:Q9RZ14; GB:AE001826; PIDN:96460827; PIDN:AAF12621.1; PID:9646 A;Experimental source: strain R1
C;Genetics:
A;Gene: DRB0144
A;Map position: megaplasmid
A;Genome: plasmid
A;Note: plasmid MP1

Query Match 61.3%; Score 38; DB 2; Length 442;
Best Local Similarity 66.7%; Pred. No. 28; Mismatches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 2 IEALPRTHE 10
Db 88 VEILPKTHE 96

RESULT 8
S40098 hypothetical protein MO1A8.2 - Caenorhabditis elegans

C;Species: *Caenorhabditis elegans*
 C;Accession: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 06-Jan-1995
 A;Reference number: A44939; MUID:90301142; PMID:2194123
 A;Accession: A44939
 A;Date: 06-Jan-1995
 A;Molecule type: mRNA
 A;Residues: 733-974, 'S', 876-916, 'S', 918-1038, 1040-1047, 'S', 1049-11283, 'E', 1285-1363 <ERO>
 A;Submitted to the EMBL Data Library, October 1993
 A;Reference number: S40998
 A;Accession: S40998
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-597 <HAW>
 A;Cross-references: EMBL:Z27081
 C;Genetics:
 A;Introns: 40/3; 76/1; 125/1; 199/1; 240/1; 274/1; 292/3; 392/3; 429/2; 486/2; 521/1
 Query Match 61.3%; Score 38; DB 2; Length 597;
 Best Local Similarity 54.5%; Pred. No. 39; Mismatches 6; Conservative 4; Gaps 0;
 Matches 1; Indels 0; Gaps 0;
 QY 2 IEALPRTHSQ 12
 DB 282 VESLQKTHETQ 292

RESULT 9
 G88551
 C;Species: *Caenorhabditis elegans*
 C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
 C;Accession: G88551
 R;anonymous: The *C. elegans* Sequencing Consortium.
 Science 282, 2012-2018, 1998
 A;Title: Genome sequence of the nematode *C. elegans*: a platform for investigating biology
 A;Reference number: A75000; MUID:99099613; PMID:9851916
 A;Note: see websites genome.wustl.edu/gsc/C_elegans/ and www.sanger.ac.uk/Projects/C_elegans/
 A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and
 A;Accession: G88551
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-893 <STO>
 A;Cross-references: UNIPROT:P34531; GB:chr_III; PIDN:CAA81607.1; PID:9387858; GSPDB:GNC
 C;Genetics:
 A;Gene: MO1A8.2
 A;Map position: 3
 Query Match 61.3%; Score 38; DB 2; Length 893;
 Best Local Similarity 54.5%; Pred. No. 60; Mismatches 6; Conservative 4; Gaps 0;
 Matches 1; Indels 0; Gaps 0;
 QY 2 IEALPRTHSQ 12
 DB 578 VESLQKTHETQ 588

RESULT 10
 T43214
 C;Species: Onchocerca volvulus
 C;Alternate names: myosin-like antigen
 C;Accession: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004
 C;Accession: T43214; AA4939; A54513; S27825
 R;Tricteeraprapab, S.; Richie, T.L.; Tuan, R.S.; Shepley, K.J.; Dinman, J.D.; Neubert, T.
 Mol. Biochem. Parasitol. 69, 161-171, 1995
 A;Title: Molecular cloning of a gene expressed during early embryonic development in *Onc*
 A;Reference number: 222341; MUID:95287898; PMID:7770081
 A;Accession: T43214
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: mRNA
 A;Residues: 1-2022 <TRI>
 A;Cross-references: UNIPROT:P21249; EMBL:U12681; NID:9530824; PID:9530825; PIDN:AA80009
 A;Experimental source: specific_host Homo sapiens
 R;Brooks, N.E.; Donelson, J.E.
 Mol. Biochem. Parasitol. 40, 213-224, 1990
 A;Title: Characterization of a myosin-like antigen from *Onchocerca volvulus*.

RESULT 11
 D83156
 molybdopterin biosynthetic protein C PA3918 [imported] - *Pseudomonas aeruginosa* (strain 1)
 C;Species: *Pseudomonas aeruginosa*
 C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 16-Aug-2004
 C;Accession: D83156
 R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warinner, P.; Hickey, M.J.; Brzadjan, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lin, J.; Lory, S.; Olson, M.V.
 Nature 406, 959-964, 2000
 A;Title: Complete genome sequence of *Pseudomonas aeruginosa* PA01, an opportunistic pathogen
 A;Reference number: A822950; MUID:20437337; PMID:10984043
 A;Accession: D83156
 A;Cross-references: UNIPROT:O9H95; GB:AE004809; GB:AE004091; NID:9950097; PIDN:AG07301
 A;Experimental source: strain PA01
 C;Genetics:
 A;Gene: moac; PA3918
 C;Superfamily: Molybdenum cofactor precursor Z biosynthesis protein Moac
 Query Match 59.7%; Score 37; DB 2; Length 160;
 Best Local Similarity 70.0%; Pred. No. 14; Mismatches 7; Conservative 1; Gaps 0;
 Matches 2; Indels 0; Gaps 0;
 QY 1 GIEALPRTHE 10
 DB 60 GIQQAKRTH 69

RESULT 12
 H81834
 hypothetical protein NMA141 [imported] - *Neisseria meningitidis* (strain Z2491 serogroup
 C;Species: *Neisseria meningitidis*
 C;Accession: H81834
 C;Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 09-Jul-2004
 C;Accession: H81834

R; Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel ; Hollond, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream, Nature 404, 502-506, 2000
 A; Title: Complete DNA sequence of a serogroup A strain of *Neisseria meningitidis* 22491.
 A; Reference number: AB1775; MUID:2022556; PMID:1076199
 A; Accession: HE1834
 A; Status: preliminary
 A; Molecule type: DNA
 A; Residues: 1-264 <PAR>
 A; Cross-references: UNIPROT:Q9JU90; GB:AL162756; GB:AL157959; NTID:g7380091; PIDN:CA8467
 A; Experimental source: serogroup A, strain 22491
 C; Genetics:
 A; Gene: NMA441
 C; Superfamily: *Neisseria meningitidis* hypothetical protein NMB1045
 Query Match 59.7%; Score 37; DB 2; Length 264;
 Best Local Similarity 50.0%; Pred. No. 25; Indels 0; Gaps 0;
 Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
 Qy 1 GIEALPRTHSQ 12
 Db 134 GLEA1ARVHKQ 145
 RESULT 13
 AR2962
 amniontransferase [imported] - *Agrobacterium tumefaciens* (strain C58, Dupont)
 C; Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
 C; Accession: AR2962
 R; Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I.; Ergec, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutyavin, T.; Levy, R.; Li, M.; McClellan, J.; Karp, P.; Romero, P.; Zhang, S. Science 294, 2317-2323, 2001
 A; Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krepan, W.; Perry, M.; Gordon-Kamm, B.; Title: The Genome of the Natural Genetic Engineer *Agrobacterium tumefaciens* C58.
 A; Reference number: AB2577; MUID:21608550; PMID:11743193
 A; Accession: AR2962
 A; Status: preliminary
 A; Molecule type: DNA
 A; Residues: 1-450 <KUR>
 A; Cross-references: UNIPROT:Q8UAS0; GB:AE008689; PIDN:AL44116.1; PID:917741685; GSPDB:G
 A; Experimental source: strain C58 (Dupont)
 C; Genetics:
 A; Gene: Atu3300
 A; Map position: linear chromosome C; Superfamily: beta-alanine-pyruvate transaminase
 Query Match 58.1%; Score 36; DB 2; Length 450;
 Best Local Similarity 70.0%; Pred. No. 69; Indels 0; Gaps 0;
 Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 Qy 2 IEALPHTHES 11
 Db 161 ITGLPRHES 170
 RESULT 14
 H98320 Family II aminotransferase [ARF247644] [imported] - *Agrobacterium tumefaciens* (strain C58 C; Species: *Agrobacterium tumefaciens*
 C; Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004
 C; Accession: H98320
 R; Goodner, B.; Hinkle, G.; Gatzung, S.; Miller, N.; Blanchard, M.; Ourollo, B.; Goldman, B.; Liu, F.; Holloman, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; Science 294, 2223-2228, 2001
 A; Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent *Agrobacterium tumefaciens*
 A; Reference number: A97339; MUID:21608551; PMID:11743194
 A; Accession: H98320
 A; Status: preliminary
 A; Molecule type: DNA
 A; Residues: 1-450 <KUR>

A; Cross-references: UNIPROT:Q8UAS0; GB:AE007870; PIDN:AAK90090.1; PID:915160077; GSPDB:G
 C; Genetics:
 A; Gene: AGR_L_3037
 A; Map position: Linear chromosome
 C; Superfamily: beta-alanine-pyruvate transaminase
 Query Match 58.1%; Score 36; DB 2; Length 450;
 Best Local Similarity 70.0%; Pred. No. 69; Indels 0; Mismatches 3; Gaps 0;
 Matches 7; Conservative 0; Gaps 0;
 Qy 2 IEALPHTHES 11
 Db 161 ITGLPRHES 170
 RESULT 15
 S52469 SOX9 protein - mouse
 C; Species: *Mus musculus* (house mouse)
 C; Date: 14-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 16-Aug-2004
 C; Accession: S52469
 R; Wright, E.; Hargrave, M.R.; Christiansen, J.; Cooper, L.; Kun, J.; Evans, T.; Gangadha Nature Genet. 9, 15-20, 1995
 A; Title: The Sry-related gene Sox9 is expressed during chondrogenesis in mouse embryos.
 A; Reference number: S52469; MUID:9521881; PMID:7704017
 A; Accession: S52469
 A; Status: preliminary
 A; Molecule type: mRNA
 A; Residues: 1-507 <WRI>
 A; Cross-references: UNIPROT:Q04887
 F; 102-177/Domain: HMG box homology <HMG1>
 Query Match 58.1%; Score 36; DB 2; Length 507;
 Best Local Similarity 41.7%; Pred. No. 78; Indels 0; Gaps 0;
 Matches 5; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
 Qy 1 GIEALPRTHSQ 12
 Db 483 GPVSIFQTHSQ 494
 RESULT 16
 A55204 transcription factor SOX9 - human
 N; Alternate names: Sex-determining region Y box 9 protein
 C; Species: *Homo sapiens* (man)
 C; Date: 27-Jan-1995 #sequence_revision 31-Dec-1995 #text_change 09-Jul-2004
 C; Accession: A55204; S50851; S52725
 R; Wagner, T.; Wirth, J.; Meyer, J.; Zabel, B.; Held, M.; Zimmer, J.; Pasantes, J.; Brica Cell 79, 111-120, 1994
 A; Title: Autosomal sex reversal and campomelic dysplasia are caused by mutations in and A; Reference number: A55204; MUID:95094274; PMID:8001137
 A; Accession: A55204
 A; Status: preliminary; not compared with conceptual translation
 A; Molecule type: DNA
 A; Residues: 1-509 <POS>
 A; Cross-references: UNIPROT:P48436; GB:S74506; NID:9807059; PIDN:AB32870.1; PID:9807060
 A; Residues: 1-509 <WAG>
 A; Cross-references: UNIPROT:P48436; GB:S74506; NID:9807059; PIDN:AB32870.1; PID:9807060
 R; Foster, J.W.; Dominguez-Steglich, M.A.; Guioli, S.; Kwok, C.; Weller, P.A.; Stevanovic Nature 372, 525-530, 1994
 A; Title: Campomelic dysplasia and autosomal sex reversal caused by mutations in an SRY-r
 R; Foster, J.W.; Dominguez-Steglich, M.A.; Guioli, S.; Kwok, C.; Weller, P.A.; Stevanovic Nature 372, 525-530, 1994
 A; Reference number: S50851; MUID:95082903; PMID:7990924
 A; Accession: S50851
 A; Status: preliminary
 A; Molecule type: mRNA
 A; Residues: 1-509 <POS>
 A; Cross-references: EMBL:246629; NID:9758102; PIDN:CAA86598.1; PID:9758103
 C; Genetics:
 A; Gene: GDB:SOX9
 A; Cross-references: GDB:134730; OMIM:211970
 A; Map position: 1q24.3-17q25.1
 C; Superfamily: unassigned HMG box proteins; HMG box homology
 P; 102-177/Domain: HMG box homology <HMG1>

Query Match	Score	DB	Length	Matches	Conservative	Mismatches	Indels	Gaps	Gap
Best Local Similarity	58.1%	DB 2;	Length 509;						
Matches	41.7%	Pred. No.	78;	5;	Conservative	4;	Mismatches	3;	Indels
Qy	1	GIEALPRTHESQ 12				0;	Gaps	0;	
Db	485	GVPSIPQTHSFQ 496							
RESULT 17									
T0932									
polyribonucleotide nucleotidyltransferase (EC 2.7.7.8) alpha chain [similarity] - Streptomyces coelicolor [misidentification]									
N;Alternate names: guanosine pentaphosphate synthetase									
C;Species: Streptomyces coelicolor									
C;Date: 05-Nov-1999 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004									
C;Accession: T10932; T05837									
R;Parkhill, J.; Barrell, B.G.; Rajandream, M.A.									
submitted to the EMBL Data Library, August 1998									
A;Reference number: T17215									
A;Accession: T10932									
A;status: translated from GB/EMBL/DDBJ									
A;Molecule type: DNA									
A;Residues: I-716 <PRO>									
A;Cross-references: UNIPROT:Q8CJ06; EMBL:AL031231; NID:93413388; PIDN:CAA20272.1; PID:93413388									
A;Experimental source: strain A3(2)									
R;Harris, D.; Taylor, K.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.									
submitted to the EMBL Data Library, August 1998									
A;Reference number: Z21590									
A;Accession: T35837									
A;status: translated from GB/EMBL/DDBJ									
A;Molecule type: DNA									
A;Residues: 603-739 <PRO>									
A;Cross-references: EMBL:AL031260; NID:93413819; PIDN:CAA20288.1; PID:93413820; GSPDB:GN									
A;Experimental source: strain A3(2)									
C;Genetics:									
A;Gene: gpsi; SCOREDB:SCA110.01									
C;Superfamily: polyribonucleotide nucleotidyltransferase									
C;Keywords: nucleotidyltransferase									
RESULT 18									
D82324									
conserved hypothetical protein VC0429 [imported] - Vibrio cholerae (strain N16961 serogroup O1; O139) #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004									
C;Species: Vibrio cholerae									
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004									
C;Accession: D82324									
R;Heidelberg, J.R.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.; chardson, D.; Brinkac, M.D.; Vamathevan, J.J.; Bibb, S.; Qin, H.; Dragoi, I.; Sellers, F.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.									
Nature 406, 477-483, 2000									
A;Title: DNA sequence of both chromosomes of the cholera pathogen Vibrio cholerae.									
A;Reference number: A82035; MUID:20406833; PMID:10952301									
A;Accession: D82324									
A;status: preliminary									
A;Molecule type: DNA									
A;Residues: 1-854 <HEI>									
A;Cross-references: UNIPROT:Q9KUT6; GB:AB004130; GB:AB003852; NID:96654845; PIDN:AABF9360									
A;Experimental source: serogroup O1; strain N16961; biotype El Tor									
C;Genetics:									
A;Gene: VC0429									
A;Map position: 1									
Query Match	58.1%	Score	36;	DB	2;	Length	854;		
Best Local Similarity	54.5%	Pred. No.	1.4e+02;						
Matches	6;	Conservative	2;	Mismatches	3;	Indels	0;	Gaps	0;
Qy	1	GIEALPRTHE 10							
Db	345	GMSGGLPRHQ 355							
RESULT 19									
A87547									
vanillin dehydrogenase [imported] - Caulobacter crescentus									
C;Species: Caulobacter crescentus									
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004									
C;Accession: A87547									
R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.F.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolonay, F.J.; Embley, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venturini, J.C.; Fraser, C.M.									
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001									
A;Title: Complete Genome Sequence of Caulobacter crescentus.									
A;reference number: A87249; MUID:21173698; PMID:11259647									
A;Accession: A87547									
A;status: preliminary									
A;Molecule type: DNA									
A;Residues: 1-470 <STO>									
A;Cross-references: UNIPROT:Q9A5PS; GB:AE005673; NID:913423939; PIDN:AAK24373.1; GSPDB:GN									
C;Genetics:									
A;Gene: CC2402									
C;Superfamily: NAD-dependent aldehyde dehydrogenase; aldehyde dehydrogenase homology									
Query Match	58.1%	Score	36;	DB	2;	Length	739;		
Best Local Similarity	60.0%	Pred. No.	1.2e+02;						
Matches	6;	Conservative	2;	Mismatches	2;	Indels	0;	Gaps	0;
Qy	2	I E A L P R T H E 11							
Db	355	VEAIPRUVHS 364							
RESULT 20									
T46576									
phosphoprotein phosphatase (EC 3.1.3.16) ppt-1 [similarity] - Neurospora crassa									
N;Alternate names: serine/threonine phosphatase PP5 homolog									
C;Species: Neurospora crassa									
C;Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 28-Apr-2003									
C;Accession: T46576									
R;Ratzka, E.; Yarden, O.									
submitted to the EMBL Data Library, February 1997									
A;Description: Ppt-1, a N. crassa novel-type phosphatase.									
A;Reference number: Z22089									
A;Accession: T46576									
A;Status: translated from GB/EMBL/DDBJ									
A;Molecule type: mRNA									
A;Residues: 1-479 <YAT>									
A;Cross-references: EMBL:UB9985; PIDN:AAB65138.1									
C;Genetics:									
A;Gene: DPT-1									
A;Map position: V									
C;Superfamily: protein phosphatase 5; phosphoprotein phosphatase									
C;Keywords: iron; metalloprotein; nucleus; phosphoric monoester hydrolase; zinc									
F;8-41/Domain: tetratricopeptide repeat homology <TT1>									
F;42-75/Domain: tetratricopeptide repeat homology <TT2>									
F;76-109/Domain: tetratricopeptide repeat homology <TT3>									
F;83-448/Domain: phosphoprotein phosphatase homology <PPP>									
F;215-284/Domain: phosphoesterase core homology <PEO>									
F;221, 223, 250/Binding site: iron (Asp, His, Asp) #status predicted									
F;282, 283, 31, 40/Binding site: zinc (Asp, Asn, His, His) #status predicted									
F;283, 283, 43/Active site: Asp, His, Tyr #status predicted									
F;254, 381/Binding site: substrate phosphate (Arg) #status predicted									
Query Match	56.5%	Score	35;	DB	1;	Length	479;		
Best Local Similarity	60.0%	Pred. No.	1.1e+02;						
Matches	6;	Conservative	3;	Mismatches	1;	Indels	0;	Gaps	0;
Qy	1	GIEALPRTHE 10							

RESULT 21	T12094	beta-fructofuranosidase (EC 3.2.1.26) - fava bean	C;Species: Vicia faba (fava bean)	C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004	R;Kaneko, T.; Sato, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda, O.; Kuroki, Y.; Asamizu, E.; Nakamura, Y.; Miyajima, N.
			C;Accession: T12094	C;Residues: 1-603 <WIL>	DNA Res. 3, 109-136, 1996
			R;Weber, H.; Borisjuk, L.; Heim, U.; Buchner, P.; Wobus, U.	A;Title: Sequence analysis of the genome of the unicellular cyanobacterium <i>Synechocystis</i> sp.	
			A;Title: Seed coat-associated invertases of Fava bean control both unloading and storage	A;Reference number: 21416; MUID:96093423; PMID:8535137	
			A;Cross-references: UNIPROT:Q43855; EMBL:235162; NID:9861154; PIDN:CAA84526.1; PID:98611	A;Accession: T12094	
			A;Experimental source: cv. Frib, seed coat	A;Status: preliminary	
			A;Genetics:	A;Accession: S74322; MUID:97061201; PMID:8905231	
			C;Gene: CWINV1	A;Status: Preliminary	
			C;Superfamily: beta-fructofuranosidase	A;Molecule type: DNA	
			C;Keywords: cell wall; glycoprotein; glycosidase; hydrolase	A;Residues: 1-603	
			Query Match 56.5%; Score 35; DB 2; Length 575; Best Local Similarity 75.0%; Pred. No. 1.4e+02; Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;	A;Cross-references: UNIPROT:Q55806; EMBL:D64004; GB:AB001339; NID:91001701; PIDN:BAA1055	
			Oy 1 GIEAPRPT 8	A;Note: the nucleotide sequence was submitted to the BMBL Data Library, June 1996	
			Db 350 GIQALPRT 357	C;Superfamily: threonine-tRNA ligase	
RESULT 22	T01575	beta-fructofuranosidase (EC 3.2.1.26) INCW2 - maize	N;Alternate names: invertase	Query Match 56.5%; Score 35; DB 2; Length 603; Best Local Similarity 77.8%; Pred. No. 1.5e+02; Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;	A;Reference number: 214354
			C;Species: Zea mays (maize)	A;Accession: T01575	
			C;Date: 19-Feb-1999 #sequence_revision 19-Feb-1999 #text_change 09-Jul-2004	A;Status: preliminary	
			C;Accession: T01575	A;Cross-references: UNIPROT:Q22187; EMBL:Z68219; PIDN:CAA92480.1; GSPPDB:GN00022; CESP:T01575	
			C;Genetics:	A;Molecule type: DNA	
			A;Gene: CESP:T05A1.3	A;Residues: 1-683 <WIL>	
			A;Map position: 4	A;Experimental source: clone T05A1	
			A;Introns: 54/3; 115/3; 165/2; 207/2; 293/2; 336/3; 375/3; 411/3; 448/3; 473/3; 531/3; 6	A;Accession: T05A1.3	
			Query Match 56.5%; Score 35; DB 2; Length 683; Best Local Similarity 70.0%; Pred. No. 1.7e+02; Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;	A;Status: preliminary; translated from GB/EMBL/DDJB	
			Oy 2 : :		
RESULT 23	S76615	hypothetical protein - <i>Synechocystis</i> sp. (strain PCC 6803)	C;Species: <i>Synechocystis</i> sp.	C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004	R;Kaneko, T.; Sato, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda, O.; Kuroki, Y.; Asamizu, E.; Nakamura, Y.; Miyajima, N.
			C;Variety: PCC 6803	C;Accession: S76615	
			C;Title: Sequence analysis of the genome of the unicellular cyanobacterium <i>Synechocystis</i> sp.	A;Title: Sequence analysis of the genome of the unicellular cyanobacterium <i>Synechocystis</i> sp.	
			C;Cross-references: UNIPROT:Q97145; PIDN:AAK79773.1; PID:915024781; GSPPDB:G	A;Cross-references: UNIPROT:Q97145; PIDN:AAK79773.1; PID:915024781; GSPPDB:G	
			A;Experimental source: Clostridium acetobutylicum ATCC824	A;Experimental source: Clostridium acetobutylicum ATCC824	
			C;Genetics:	C;Genetics:	
			A;Gene: CACI808	A;Gene: CACI808	
			C;Superfamily: polyribonucleotide nucleotidyltransferase	C;Superfamily: polyribonucleotide nucleotidyltransferase	

Query Match 55.5%; Score 35; DB 2; Length 703;
 Best Local Similarity 60.0%; Pred. No. 1.7e+02; PIDN:AAC13941.1; GSPDB:GNK
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 2 IEALPRTHES 11
 Db 328 VDULPRTHES 337

RESULT 26

A77069 hypothetical protein PH1246 - Pyrococcus horikoshii
 C;Species: Pyrococcus horikoshii
 C;Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 09-Jul-2004
 C;Accession: A71069
 R;Kawarabayashi, Y.; Sawada, M.; Horikawa, H.; Hikawa, Y.; Hino, M.; Onishi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguchi, M.; Ohfuki, Y.; Funahashi, T.; Nakamura, S.; Sekine, A.; Title: Complete sequence and gene organization of the genome of a hyper-thermophilic archaeon, Pyrococcus horikoshii, strain OR3, ATCC 70076. Reference number: A71000; MUID:98344137; PMID:9679194
 A;Status: preliminary; nucleic acid sequence not shown; translation not shown
 A;Molecule type: DNA
 A;Residues: 1-727 <KUR>
 A;Cross-references: UNIPROT:058935; GB:AP000005; NID:93236132; PIDN:BA00347.1; PID:dl03
 A;Experimental source: strain OR3
 A;Note: this accession replaces an interim accession for a sequence replaced by GenBank
 C;Genetics: A;Gene: PH1246

RESULT 27

Query Match 55.5%; Score 35; DB 2; Length 727;
 Best Local Similarity 60.0%; Pred. No. 1.8e+02; PIDN:AA02093; NID:94803947; PIDN:AAD29820.1; GSPDB:GNK
 Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GIEALPRTHE 10
 Db 649 GIEALPGTYQ 658

RESULT 28

H90607 Query Match 55.5%; Score 35; DB 2; Length 727;
 Best Local Similarity 60.0%; Pred. No. 1.8e+02; PIDN:AA02093; NID:94803947; PIDN:AAD29820.1; GSPDB:GNK
 Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GIEALPRTHE 10
 Db 649 GIEALPGTYQ 658

RESULT 29

D66902 hypothetical protein b1489 - Escherichia coli (strain K-12)
 C;Species: Escherichia coli
 C;Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 16-Aug-2004
 C;Accession: H90607
 R;Chambaud, I.; Heilig, R.; Ferris, S.; Barbe, V.; Samson, D.; Galisson, F.; Moszer, I.; A.; Title: The complete genome sequence of the murine respiratory pathogen Mycoplasma pulmonis. Reference number: A99512; MUID:21267165; PMID:11353084
 A;Accession: H90607
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-741 <KUR>
 A;Cross-references: UNIPROT:Q98PFS; GB:AL445566; PID:914090183; PIDN:CA00347.1; GSPDB:GNK
 A;Experimental source: strain UAB CTIP
 C;Genetics:
 A;Gene: MYPU_7680
 A;Genetic code: SGC3
 C;Superfamily: helicase II

Query Match 55.5%; Score 35; DB 2; Length 741;
 Best Local Similarity 54.5%; Pred. No. 1.8e+02; PIDN:AA02093; NID:94803947; PIDN:AAD29820.1; GSPDB:GNK
 Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GIEALPRTHES 11
 Db 725 GIEALPRTHES 735

RESULT 30

AFF1082 B. subtilis Yuka protein homolog lmc0061 [imported] - Listeria monocytogenes (strain EGD
 C;Species: Listeria monocytogenes
 C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
 C;Accession: AF1082
 R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecher, A.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fehl, H.; Jones, L.M.; Karst, U.; Science 294, 849-852, 2001
 A;Authors: Kraft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitouram, A.; Mai, C.; Schlueter, T.; Simoes, N.; Tierre, A.; Vazquez-Boland, J.A.; Voss, H.; Weiland, A.; Title: Comparative genomics of Listeria species.
 A;Reference number: AB1077; MUID:21537279; PMID:11679669
 A;Accession: AF1082
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-1498 <GLA>
 A;Cross-references: UNIPROT:Q8YHQ5; GB:NC_003210; PIDN:CAC98276.1; PID:916409420; GSPDB:GNK
 C;Species: Arabidopsis thaliana (mouse-ear cress)

RESULT 28

D84595 pearl 4 protein [imported] - Arabidopsis thaliana
 A;Cross-references: UNIPROT:Q8YHQ5; GB:NC_003210; PIDN:CAC98276.1; PID:916409420; GSPDB:GNK

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A;Experimental source: strain EGD-e
C;Genetics:
A;Gene: lmo0661

Query Match 56.5%; Score 35; DB 2; Length 1498;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 7; Conservative 0; Mismatches 0;
Indels 0; Gaps 0;
QY 1 GIEALPR 7
| |||||
Db 941 GIEALPR 947

Search completed: August 1, 2005, 08:49:02
Job time : 44 secs

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GenCore version 5.1.6
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OM protein - protein search, using bw model

Run on: August 1, 2005, 08:26:18 ; Search time 173 Seconds
(without alignments)
35.520 Million cell updates/sec

Title: US-10-663-749-18
Perfect score: 62
Sequence: 1 GIEALPRTHESQ 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext: 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 150 summaries

Database : UniProt_03:
1: uniprot_sprot:
2: uniprot_trembl:
*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	#	Match Length	DB ID	Description
1	62	100.0	500	1	PTG1_HUMAN	Q16647 homo sapien
2	62	100.0	500	2	O6LEN2	O6len2 homo sapien
3	62	100.0	509	2	O6LEN0	O6len0 homo sapien
4	55	88.7	168	2	Q7TSX2	mus musculus
5	55	88.7	501	1	PTG1_MOUSE	O35074 mus musculus
6	55	88.7	501	1	PGC1_MOUSE	Q62659 ratmus norvegicus
7	55	88.7	509	2	O8BXCO	O8bxco mus musculus
8	43	69.4	1534	2	Q7QTR2	Q7qt2 giardia lamblia
9	42	67.9	310	2	O6MLK6	O6mlk6 bacillus
10	41	66.1	134	2	O865C7	O865c7 capra hircus
11	41	65.1	500	1	PTG1_BOVIN	O2926 bos taurus
12	41	60.1	802	2	Q87L51	Q87l51 vibrio para
13	40	64.5	399	2	O92M18	O92m18 rhizobium m
14	40	64.5	880	2	O9SVU3	O9svu3 arabidopsis thaliana
15	40	64.5	924	2	O949M4	O949m4 arabidopsis thaliana
16	40	64.5	2530	2	O6RKG3	O6rk33 mycosphaerellaceae
17	39	62.9	248	2	O87XK6	O87xk6 pseudomonas
18	39	62.9	271	2	O8V4P7	O8v4p7 dictyostelia
19	39	62.9	283	2	O87QG9	O87qg9 vibrio para
20	39	62.9	294	2	O6CKA0	O6cka0 kluveromyces
21	39	62.9	310	2	O73YB1	O73yb1 mycobacterium
22	39	62.9	364	2	O6A8K2	O6a8k2 propionibacter
23	39	62.9	367	2	O8XAUB	O8xaub escherichia
24	39	62.9	400	2	O86L11	O86l11 dictyostelia
25	39	62.9	408	2	O9HC82	O9hc82 homosapiens
26	39	62.9	1001	2	O6AHZ6	O6ahz6 homo sapiens
27	39	62.9	1001	2	O7LJ3T6	O7lj3t6 homo sapiens
28	39	62.9	1030	2	O75150	O75150 homo sapiens
29	38	61.3	127	2	O7YU66	O7yu66 trypanosoma
30	38	61.3	310	2	O8CIIA	O8ci14 mus musculus
31	38	61.3	350	2	O923H4	O923h4 mus musculus

Q92Z14 deinococcus radiodurans
Q91FB5 homo sapien
Q91358 homo sapien
Q9Y5B0 rattus norvegicus
Q8B9G5 mus musculus
Q8u93 lactobacillus
Q729M0 trichoderma
Q652C5 caenorhabditis elegans
P34531 caenorhabditis elegans
Q8WZT2 neurospora crassa
P2249 onchocerca
Q91X95 pseudomonas aeruginosa
Q73uA7 mycobacterium tuberculosis
Q83GA6 tropheryma thermophila
Q83NN0 tropheryma thermophila
Q91u90 neisseria meningitidis
Q7dzz7 anophelles gambiae
Q919Z9 drosophila melanogaster
Q7pkv2 anophelles gambiae
Q7ka83 desulfobacter
Q25586 onchocerca
Q6ee02 reovirus type 2
Q6Lvn4 photobacterium
Q9u82 gaeumannomyces tritici
Q8182 plasmoidium
Q8183 plasmoidium
Q8189 desulfobacter
Q7ur68 rhodopirellus
Q9F6X4 pseudomonas
Q8K0S2 ralstonia
Q9lb78 gallus gallus
Q9vzw4 drosophila melanogaster
Q67P85 symbiota sativum
Q7xe2 oryzopsis
Q8uas0 agrobacteriaceae
Q6dft5 xenopus laevis
Q90Y11 xenopus laevis
Q76K22 streptococcus
Q6F2E7 xenopus tropicalis
Q61n79 rana rugosa
Q9de28 eublepharis kuroiwae
Q73668 gallus gallus
Q9YGP7 alligator mississippiensis
Q04887 mus musculus
P48436 homo sapien
P61753 macaca mulatta
Q9b9B9 pan troglodytes
Q18836 sub scrofa
P61754 pongo pygmaeus
Q9bb91 callithrix jacchus
Q9bg92 hylobates
Q6N6F2 rhodopseudomonas
Q7YrJ7 canis familiaris
Q6dd25 xenopus laevis
Q8P669 methanobacter
Q8dw21 streptococcus
Q8E202 streptococcus
Q7QF13 amorphophallus
Q6F114 candida glabrata
Q7qq36 giardia lamblia
Q7XH39 otzyva sativa
Q86gh5 amorphophallus
Q9nkV3 bombyx mori
Q82180 streptomyces
Q8Cj96 streptomyces
Q53597 streptomyces
Q9kt6 vibrio cholerae
Q9ir3 caenorhabditis elegans

DR Pfam; PR0067; P450; 2.
 DR PRINTS; PR0045; EP450IV.
 DR PROSITE; PR0086; CYTOCHROME_P450; FALSE_NEG.
 KW Endoplasmic reticulum; Heme; Isomerase; Polymorphism;
 KW prostaglandin biosynthesis; Transmembrane.
 FT TRANSMEM 1 20
 FT METAL 441 441 Iron (heme axial ligand) (By similarity).
 FT VARIANT 38 38 /FTId=VAR 010915.
 FT VARIANT 118 118 S --> R (in allele CYP8A1*3; dbSNP:5622).
 FT VARIANT 154 154 /FTId=VAR 010916.
 FT VARIANT 171 171 E --> A (in dbSNP:5623).
 FT VARIANT 236 236 /FTId=VAR 014634.
 FT VARIANT 379 379 F --> L (in dbSNP:5624).
 FT VARIANT 500 500 /FTId=VAR 014635.
 FT VARIANT 500 AA; 57103 MW; 39595442BFC0B625 CRC64;
 SQ SEQUENCE 500 AA; 57131 MW; 9DCC11CF771C3BED CRC64;

Query Match Best local Similarity 100.0%; Score 62; DB 1; Length 500;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 GIEALPRTHESQ 12
 Db 182 GIEALPRTHESQ 193

RESULT 2

Q6LEN2 PRELIMINARY; PRT; 500 AA.
 ID Q6LEN2; AC Q6LEN2; DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
 DB Prostacyclin synthase (EC 5.3.99.4).
 GN Name=PTGIS(CP8);
 OS Homo sapiens (Human);
 OC Eukaryota; Merazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1] SEQUENCE FROM N.A.
 RX MEDLINE-94242046; PubMed=8185632;
 RA Miyata A., Hara S., Yokoyama C., Inoue H., Ulrich V., Tanabe T.;
 RT "Molecular cloning and expression of human Prostacyclin synthase.";
 RL Biochem. Biophys. Res. Commun. 200:1728-1734(1994).
 RN [2] SEQUENCE FROM N.A.
 RX MEDLINE-96411687; PubMed=8812456; DOI=10.1006/geno.1996.0465;
 RA Yokoyama C., Yabuki T., Inoue H., Tone Y., Hara S., Hatae T.,
 RA Nagata M., Takahashi E.-I., Tanabe T.;
 RT "Human gene encoding prostacyclin synthase (PTGIS): genomic organization, chromosomal localization, and promoter activity.";
 RT Genomics 36:296-304(1996).
 RN [3] SEQUENCE FROM N.A.
 RP Submitted (FEB-1996) to the EMBL/GenBank/DBBJ databases.
 RL - - SIMILARITY: Belongs to the cytochrome P450 family.
 EMBL; D83393; BAA11910.1; JOINED.
 EMBL; D83394; BAA11910.1; JOINED.
 EMBL; D83395; BAA11910.1; JOINED.
 EMBL; D83396; BAA11910.1; JOINED.
 EMBL; D83397; BAA11910.1; JOINED.
 EMBL; D83398; BAA11910.1; JOINED.
 EMBL; D83399; BAA11910.1; JOINED.
 EMBL; D83400; BAA11910.1; JOINED.

DR EMBL; DB3401; BAA11910.1; JOINED.
 DR EMBL; DB3402; BAA11910.1; .-.
 GO; GO:0016053; F-isomerase activity; IEA.
 GO; GO:0004937; F-monoxygenase activity; IEA.
 GO; GO:0008116; F-prostaglandin-I synthase activity; IEA.
 DR InterPro; IPR001128; Cytochrome_P450.
 DR InterPro; IPR002403; EP450IV.
 DR PRINTS; PR0045; EP450IV.
 DR PRINTS; PR0038; P450.
 KW CYCLIN; Heme; Isomerase.
 SQ SEQUENCE 500 AA; 57131 MW; 9DCC11CF771C3BED CRC64;

Query Match Best local Similarity 100.0%; Score 62; DB 2; Length 500;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 GIEALPRTHESQ 12
 Db 182 GIEALPRTHESQ 193

RESULT 3

Q6LEN0 PRELIMINARY; PRT; 509 AA.
 ID Q6LEN0; AC Q6LEN0; DT 05-JUL-2004 (TREMBLrel. 27, Created)
 DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
 DE Prostacyclin synthase (EC 5.3.99.4) (Fragment).
 OG Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1] SEQUENCE FROM N.A.
 RC STRAIN=Japanese; TISSUE=Leucocyte;
 RX MEDLINE-96203537; PubMed=8630042; DOI=10.1006/bbrc.1996.0677;
 RA Nakayama T., Soma M., Izumi Y., Kamatsuse K.;
 RT "Organization of the human prostacyclin synthase gene.";
 RL Biochem. Biophys. Res. Commun. 221:803-806(1996).
 CC !-- SIMILARITY: Belongs to the cytochrome P450 family.
 DR EMBL; D84115; BAA28219.1; JOINED.
 DR EMBL; D84116; BAA28219.1; JOINED.
 DR EMBL; D84117; BAA28219.1; JOINED.
 DR EMBL; D84118; BAA28219.1; JOINED.
 DR EMBL; D84119; BAA28219.1; JOINED.
 DR EMBL; D84120; BAA28219.1; JOINED.
 DR EMBL; D84121; BAA28219.1; JOINED.
 DR EMBL; D84122; BAA28219.1; JOINED.
 DR EMBL; D84123; BAA28219.1; JOINED.
 DR EMBL; D84124; BAA28219.1; .-.
 DR GO; GO:0016853; F-isomerase activity; IEA.
 DR GO; GO:0004497; F-monoxygenase activity; IEA.
 DR GO; GO:0008116; F-prostaglandin-I synthase activity; IEA.
 DR GO; GO:0006118; P:electron transport; IEA.
 DR InterPro; IPR001128; Cytochrome_P450.
 DR InterPro; IPR002403; EP450IV.
 DR PRINTS; PR0045; EP450IV.
 DR PRINTS; PR0038; P450.
 KW CYCLIN; Heme; Isomerase.
 SQ SEQUENCE 509 AA; 57869 MW; 200FF90BFF62EBCE CRC64;

Query Match Best local Similarity 100.0%; Score 62; DB 2; Length 509;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 GIEALPRTHESQ 12
 Db 191 GIEALPRTHESQ 202

RESULT 4	Q7PSX2	PRELIMINARY;	PRT;	168 AA.
ID	OTTSX2;			
RC	01-OCT-2003 (TREMBIREL, 25, Created)			
RC	01-OCT-2003 (TREMBIREL, 25, Last sequence update)			
DT	01-MAR-2004 (TREMBIREL, 26, Last annotation update)			
DE	Prostacyclin synthase (Fragment).			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OC	NCBI_TaxID=10990;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=Kunning;			
RA	Ding N.-Z., He C.-Q., Yang Z.-M.;			
RA	Submitted (APR-2003) to the cytochrome P450 family.			
CC	-1-SIMILARITY: Belongs to the cytochrome P450 family.			
EMBL	AY285779; AM374451; -;			
FT	SEQUENCE FROM N.A.			
DR	GO:0006118; P:electron transport; IBA.			
DR	Interpro; IPR01128; Cytochrome_P450.			
DR	Pfam; PF0067; P450; 1.			
KW	Cylin; Hemeoxygenase; Oxidoreductase.			
FT	NON_TER			
FT	SEQUENCE			
SQ	168 AA; 1886 MW; 59E78F4B4FE6690B CRC64;			
Query Match	88 %;	Score 55;	DB 2;	Length 168;
Best Local Similarity	83.3 %;	Pred. No. 0.024;	1;	Indels 0; Gaps 0;
Matches	10;	Conservative 1;	Mismatches 1;	
QY	1 GIEALPRTHSQ 12			
Db	5 GVEASPRTHESQ 16			
RESULT 5				
PTGI_MOUSE	STANDARD;	PRT;	501 AA.	
AC	Q35074;			
DT	16-OCT-2001 (Rel. 40, Last sequence update)			
DT	16-OCT-2004 (Rel. 45, Last annotation update)			
DE	Prostacyclin synthase (EC 5.3.99.4) (prostaglandin H2 to GN Name=PgS; Synonyms=CYP8;			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OC	NCBI_TaxID=10990;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=C57BL/6J; TISSUE=peritoneal macrophage;			
RX	MEDLINE:9734562; PubMed=9202154; DOI=10.1016/S0014-5793(97)00516-4;			
RA	Kuwamoto S., Inoue H., Tone Y., Izumi Y., Tanabe T.;			
RT	"Inverse gene expression of prostacyclin and thromboxane synthases in resident and activated peritoneal macrophages";			
RT	FEBS Lett. 409:242-246(1997).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=C57BL/6J; TISSUE=Testis;			
RX	MEDLINE:2235663; PubMed=12466851; DOI=10.1038/nature01266;			
RA	Nikaido I., Osato N., Saito R., Suzuki H., Yamamoto I., Kiyosawa H., Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T., Okazaki Y., Furukawa T., Kasukawa T., Adachi J., Bono H., Kondo S., Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J., Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W., Blake J.A., Bradt D., Busick V., Chothia C., Corbeni L.E., Cousins S., Dalla E., Dragni T.A., Fletcher C.P., Forrest A., Prater K.S.,			
RA	Draeger J., Jackson I.J., Jarvis E.D., Grimmond S., Gustincich M., Hirakawa N., Jackson J., Keddie R.M., King B.L., Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A., Magliott D.R., Maitais L., Marchionni L., McKenzie L., Miki H., Nagashima T., Nunata K., Okido T., Pavon W.J., Pertea G., Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S., Ravasi T., Reed J.C., Reed J.J., Ring B.Z., Ringwald M., Sandelin A., Schneide C., Simple C.A., Setou M., Shimada K., Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M., Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C., Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N., Hirozane-Kishikawa T., Konno H., Nakamura M., Sakakuni N., Satoh T., Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S., Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I., Miyazaki A., Sakai K., Sasaki D., Shitara K., Shinagawa A., Yasunishi A., Yoshino M., Watterston R., Lander E.S., Rogers J., Birney E., Hayashizaki Y.,			
RA	Birney E., Hayashizaki Y., "Analysis of the mouse transcriptome based on functional annotation of full-length cDNAs"; Nature 420:563-573(2002).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Limb;			
RX	MEDLINE:22388257; PubMed=12477932; DOI=10.1073/pnas.242603999;			
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmim C.M., Schuler G.D., Atschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhak N.K., Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Clegg C., Raha S.S., Loqueland N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunnarine P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Farley J., Heitton E., Kettman M., Madan A., Rodrigues S., Sanchez A., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalius D.E., Schnurch A., Schein J.E., Jones S.J.M., Marra M.A., "Generation and initial analysis of more than 15,000 full-length human RT and mouse cDNA sequences"; Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).			
RT	-1-FUNCTION: Catalyzes the isomerization of prostaglandin H2 to prostacyclin (=prostaglandin I2).			
CC	-1-CATALYTIC ACTIVITY: (5Z,13E)-(15S)-9-alpha,11-alpha-epidioxy-15-hydroxyprosta-5,13-dienoate = (5Z,13E)-(15S)-6,9-alpha-epoxy-11-alpha,15-dihydroxyprosta-5,13-dienoate.			
CC	-1-SUBCELLULAR LOCATION: Endoplasmic reticulum membrane. May be anchored to the membrane via a single transmembrane domain.			
CC	-1-SIMILARITY: Belongs to the cytochrome P450 family.			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce or send an email to license@isb-sib.ch).			
CC	EMBL; AB001607; BRA21717.1; -;			
CC	EMBL; AK076585; BAC36403.1; -;			
CC	EMBL; BC062151; AAH62151.1; -;			
CC	MGD; MGJ:1091156; Ptgs.			
CC	InterPro; IPR001128; Cytochrome_P450.			
CC	InterPro; IPR02403; EP450IV.			
CC	PRINTS; PR00465; EP450IV.			
CC	PRINTS; PR00385; P450.			
CC	PROSITE; PS00086; CYTOCHROME_P450; FALSE NEG.			

KW Endoplasmic reticulum; Heme; Isomerase; Prostaglandin biosynthesis;
KW Transmembrane.

FT TRANSMEM 1 21 Potential.

FT METAL 442 442 Iron (heme axial ligand) (By similarity).

SEQUENCE 501 AA; 57046 MW; F018F85D3A1B0EBB CRC64;

Query Match 88.7%; Score 55; DB 1; Length 501;
Best local Similarity 83.3%; Pred. No. 0.077; 1; Mismatches 10; Conservative 1; Indels 0; Gaps 0;

Oy 1 GIEALPRTRSQ 12
Db 183 GVEASPRTHESQ 194

RESULT 6

ID	PGC1_RAT	STANDARD:	PRT:	501 AA.																																																																																																																																																																																																																																																																																																																																	
AC	062969;																																																																																																																																																																																																																																																																																																																																				
DT	16-OCT-2001 (Rel. 40, created)																																																																																																																																																																																																																																																																																																																																				
DT	16-OCT-2001 (Rel. 40, last sequence update)																																																																																																																																																																																																																																																																																																																																				
DT	01-MAR-2004 (Rel. 44, last annotation update)																																																																																																																																																																																																																																																																																																																																				
DE	Prostagacyclin synthase (EC 5.3.99.4) (Prostaglandin I2 synthase).																																																																																																																																																																																																																																																																																																																																				
GN	Name=Ptg1; Synonyms=Cpt1b;																																																																																																																																																																																																																																																																																																																																				
OS	Rattus norvegicus (Rat);																																																																																																																																																																																																																																																																																																																																				
OC	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;																																																																																																																																																																																																																																																																																																																																				
OC	Mammalia; Eutheria; Rodentia; Sciuromorpha; Muridae; Murinae; Rattus.																																																																																																																																																																																																																																																																																																																																				
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RP	SEQUENCE FROM N.A.																																																																																																																																																																																																																																																																																																																																				
RA	Geraci M.W., Gao B., Shepherd D., Moore M., Vernon J., Miller Y.E.,																																																																																																																																																																																																																																																																																																																																				
RA	Vogelkel N.F.;																																																																																																																																																																																																																																																																																																																																				
RL	Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.																																																																																																																																																																																																																																																																																																																																				
CC	-1- FUNCTION: Catalyzes the isomerization of prostaglandin H2 to prostacyclin (=prostaglandin I2) (By similarity).																																																																																																																																																																																																																																																																																																																																				
CC	-1- CATALYTIC ACTIVITY: (5Z,13E)-(15S)-9-alpha,11-alpha-epidioxy-15-hydroxyprosta-5,13-dienoate = (5Z,13E)-(15S)-6,9-alpha-epoxy-11-alpha,15-dihydroxyprosta-5,13-dienoate.																																																																																																																																																																																																																																																																																																																																				
CC	-1- SUBCELLULAR LOCATION: Endoplasmic reticulum membrane. May be anchored to the membrane via a single transmembrane domain.																																																																																																																																																																																																																																																																																																																																				
CC	-1- SIMILARITY: Belongs to the cytochrome P450 family.																																																																																																																																																																																																																																																																																																																																				
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).																																																																																																																																																																																																																																																																																																																																				
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CC	EMBL; U53855; ARB02322.1; -.																																																																																																																																																																																																																																																																																																																																				
DR	EMD; 3438; Ptgsb.																																																																																																																																																																																																																																																																																																																																				
DR	InterPro; IPR001128; Cytochrome_P450.																																																																																																																																																																																																																																																																																																																																				
DR	InterPro; IPR002403; EP450IV.																																																																																																																																																																																																																																																																																																																																				
DR	PFAM; PF00067; P450; 2.																																																																																																																																																																																																																																																																																																																																				
DR	PRINTS; PR0045; EP450IV.																																																																																																																																																																																																																																																																																																																																				
DR	PROSITE; PS00385; P450.																																																																																																																																																																																																																																																																																																																																				
DR	Endoplasmic reticulum; Heme; Isomerase; Prostaglandin biosynthesis; Transmembrane.																																																																																																																																																																																																																																																																																																																																				
FT	TRANSMEM 1 21 Potential.																																																																																																																																																																																																																																																																																																																																				
FT	METAL 442 442 Iron (heme axial ligand) (By similarity).																																																																																																																																																																																																																																																																																																																																				
SEQUENCE 501 AA; 57127 MW; D2b85ADF5C464863 CRC64; <p>Query Match 88.7%; Score 55; DB 1; Length 501; Best Local Similarity 83.3%; Pred. 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RC	Adachi J., Alzawa K., Atsumura T., Arakawa T., Bono H., Carninci P.,																																																																																																																																																																																																																																																																																																																																				
RA	Fukuda S., Furuno M., Hanagata N., Hiramoto K., Hirokawa T., Hirozane T.,																																																																																																																																																																																																																																																																																																																																				
RA	Hayashida K., Hayatsu N., Hiramoto K., Hirokawa T.,																																																																																																																																																																																																																																																																																																																																				
RA	Hori F., Imotani K., Ishii Y., Ichijo M., Kagawa I., Kasukawa T.,																																																																																																																																																																																																																																																																																																																																				
RA	Katoh H., Kawai J., Kohji Y., Kondo S., Kondo H., Kouda M., Koya S.,																																																																																																																																																																																																																																																																																																																																				
RA	Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,																																																																																																																																																																																																																																																																																																																																				
RA	Nishi K., Nomura K., Numasaki R., Ohno M., Obata N., Okazaki Y.,																																																																																																																																																																																																																																																																																																																																				
RA	Saito R., Saitoh H., Sakai C., Sahai K., Sakazume N., Sano H.,																																																																																																																																																																																																																																																																																																																																				
RA	Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,																																																																																																																																																																																																																																																																																																																																				
RA	Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,																																																																																																																																																																																																																																																																																																																																				

RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 CC -I- SIMILARITY: Belongs to the cytochrome P450 family.
 DR EMBL; AK048059; BAC33227.1; -.
 DR MGII; MGII:197156; Ptgs.
 DR GO; GO:0005615; Clextracellular space; TAS.
 DR InterPro; IPR001128; Cytochrome_P450.
 DR InterPro; IPR002403; EP450IV.
 DR PTAN; PTAN067; P450; 2.
 DR PRINTS; PR00365; EP450IV.
 DR PRINTS; PR00385; P450.
 KW Cyclin; Heme.

SQ SEQUENCE 509 AA; 57769 MW; 732B51B854E70002 CRC64;
 Query Match 88.7%; Score 55; DB 2; Length 509;
 Best Local Similarity 83.3%; Pred. No. 0.078;
 Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 GIEALPRTHESQ 12
 Db 183 GVEASPRTHESQ 194

RESULT 8

Q7QTR2 PRELIMINARY; PRT; 1534 AA.
 ID Q7QTR2
 AC Q7QTR2
 DT 01-MAR-2004 (TREMBLrel. 26, Created)
 DT 01-MAR-2004 (TREMBLrel. 26, Last sequence update)
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
 DB GLP 510 27846 23242.
 OS Giardia lamblia ATCC 50803.
 OC Buxaryota; Diplomonadida; Hexamitidae; Giardinae; Giardia.
 NCBI_TaxID=184922;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NWB C6;
 RA Morrison H.G., McArthur A.G., Adam R.D., Aley S.B., Gillin F.D.,
 RA Olsen G.J., Sogin M.L.;
 RT "Draft sequence of the Giardia lamblia genome.";
 RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
 CC -I- CAUTION: The sequence shown here is derived from an
 EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 preliminary data.
 DR EMBL; AACB01000102; EAM38417.1; -.
 SEQUENCE 1534 AA; 171028 MW; 41A7BB9C9CAC36CF CRC64;

Query Match 69.4%; Score 43; DB 2; Length 1534;
 Best Local Similarity 72.7%; Pred. No. 54;
 Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 Qy 2 IEALPRTHESQ 12
 Db 1300 IAMPRTTHESQ 1310

RESULT 9

Q6MLK6 PRELIMINARY; PRT; 310 AA.
 ID Q6MLK6
 AC Q6MLK6;
 DT 05-JUL-2004 (TREMBLrel. 27, Created)
 DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
 DE Hypothetical transmembrane protein yneB.
 GN Name=yneB; OrderedProteinNames=Bd2002;
 OS Bdellovibrio bacteriovorus.
 OC Bacteria; Proteobacteria; Betaproteobacteria; Bdellovibrionales;
 OC Bdellovibrionaceae; Bdellovibrio.
 OK NCBI_TaxID=959;
 RN [1]
 SEQUENCE FROM N.A.

RP STRAIN=HD100 / DSM 50701 / ATCC 15356 / NCIB 9529;
 RC PubMed=14752164; DOI=10.1126/science.1093027;

Rendulic S., Jagtap P., Rosinus A., Eppinger M., Baar C., Lanz C.,
 RA Keller H., Lambert C., Evans K.J., Goessmann A., Meyer F.,
 RA Schuster R.E., Schuster S.C.;
 RT "A predator unaware: Life cycle of Bdellovibrio bacteriovorus from a
 genomic perspective." Science 303:689-692 (2004).
 RL EMBL; BX842651; CAB79851.1; -.
 DR InterPro; IPR007913; UPF0187.
 DR Pfam; PF05249; UPF0187; 1.
 KW Complete proteome.

SQ SEQUENCE 310 AA; 35262 MW; C469B4820D2A2A38 CRC64;
 Query Match 67.7%; Score 42; DB 2; Length 310;
 Best Local Similarity 66.7%; Pred. No. 15;
 Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 Qy 1 GIEALPRTHESQ 12
 Db 295 GEKALPRNHEGQ 306

RESULT 10

Q865C7 PRELIMINARY; PRT; 134 AA.
 ID Q865C7
 AC Q865C7;
 DT 01-JUN-2003 (TREMBLrel. 24, Created)
 DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)
 DE Prostacyclin Synthase (Fragment).
 OS Capra hircus (Goat).
 OC Buxaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
 Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 Caprinae; Capra.
 NCBI_TaxID=9925;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Kawate N., Truji M., Tamada H., Inaba T., Sawada T.;
 RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY221118; AA065922.1; -.
 KW CYCLIN.
 FT NON_TER 1
 PT NON_TER 134 134
 SQ SEQUENCE 134 AA; 15105 MW; F7FF03CACBDAD6C4 CRC64;
 Query Match 66.1%; Score 41; DB 2; Length 134;
 Best Local Similarity 66.7%; Pred. No. 9.4;
 Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 Qy 1 GIEALPRTHESQ 12
 Db 46 GVEAPPHIOESQ 57

RESULT 11

PTGI_BOVIN STANDARD; PRT; 500 AA.
 ID PTGI_BOVIN
 AC Q29626; Q28841;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Prostacyclin synthase (EC 5.3.99.4) (prostaglandin D2 synthase).
 Name=PTGS; Synonyms=CYP8;
 OS Bos taurus (Bovine).
 OC Buxaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
 Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 Caprinae; Bos.
 NCBI_TaxID=9913;
 RN [1]
 SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.

RC TISSUE-Aorta;
 RX MEDLINE-B9437536; PubMed=8451072;
 RA Hara S., Miyata A., Yokoyama C., Inoue H., Brugge R., Lottspeich F.,
 RA Ulrich V., Tanabe T.;

DR GO: GO:006810; P:transport; IEA.
 DR InterPro; IPR04812; Efflux_Bcr_Cfia.
 DR TIGRFAMS; TIGR0710; efflux_Bcr_Cfia; 1.
 DR PROSITE; PS5085; MFS; 1.
 DR KW Complete proteome; Transmembrane.
 SQ SEQUENCE 399 AA; 42519 MW; CD4E743D34BDC89 CRC64;
 Query Match 64.5%; Score 40; DB 2; Length 399;
 Best Local Similarity 63.6%; Pred. No. 48;
 Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
 QY 2 REALRTHESQ 12
 DB 184 LQALPRWHESR 194

RESULT 14

QSYVU3 PRELIMINARY; PRT; 880 AA.
 AC QSYVU3;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
 DE Hypothetical protein FLGA16_130 (Hypothetical protein AT4928760).
 GN Name=F1616_130; Synonym=AT4928760;
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicots; rosids;
 OC eurosid II; Brassicales; Brassicaceae; Arabidopsis.
 OC eurosid II; Brassicaceae; Arabidopsis.
 OX NCBI_TAXID=3702;
 RN [1] SEQUENCE FROM N.A.
 RP Bevan M., Brandt P., Dose S., Jarke D., Scharfe M., Schon O.,
 RA Honeisel J., Mewes H.W., Mayer K.F.X., Schneller C.;
 RL Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RL Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Brandt P., Dose S., Jarke D., Scharfe M., Schon O., Mewes H.W.,
 RA Lemke K., Mayer K.F.X.;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RA EU Arabidopsis sequencing project;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AL03535; CAA22961; -.
 DR EMBL; AL161573; CAB881464; 1; -.
 DR PIR; T0523; T04523.
 KW Hypothetical protein.
 SQ SEQUENCE 880 AA; 98423 MW; SF01102587BCBBFO CRC64;

Query Match 64.5%; Score 40; DB 2; Length 880;
 Best Local Similarity 60.0%; Pred. No. 1.1e+02;
 Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 GIEALPRTHE 10
 DB 118 GLERILPQHQ 127

RESULT 16

Q6RKG3 PRELIMINARY; PRT; 2530 AA.
 AC Q6RKG3;
 DT 05-JUL-2004 (TREMBLrel. 27, Created)
 DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
 DE Polyketide synthase.
 GN Name=PKS1;
 OS Mycosphaerella zeae-maydis.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina;
 OC Dothideomycetes et Chaetothyriomycetidae incertae sedis;
 OC Mycosphaerellaceae; Mycosphaerella.
 OX NCBI_TAXID=259522;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX PubMed:1467319; DOI=10.1073/pnas.2532165100;
 RA Kroken S., Glass N.L., Taylor J.W., Yoder O.C., Turgeon B.G.;
 RT "Phylogenomic analysis of type I polyketide synthase genes in
 pathogenic and saprobic ascomycetes";
 RL Proc. Natl. Acad. Sci. U.S.A. 100:15670-15675 (2003).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Yun S.-Y., Turgeon B.G.;
 RL Submitted (DEC-2003) to the EMBL/GenBank/DDBJ databases.
 DR GO; GO:0004024; P:alcohol dehydrogenase activity, zinc-dependent; IEA.
 DR GO; GO:0048037; P:cofactor binding; IEA.
 DR GO; GO:0016740; P:transferase activity; IEA.
 DR GO; GO:0008870; P:zinc ion binding; IEA.
 DR GO; GO:0006333; P:fatty acid biosynthesis; IEA.
 DR GO; GO:008152; P:metabolism; IEA.
 DR InterPro; IPR009081; ACP_like.

RESULT 15

Q949M4 PRELIMINARY; PRT; 924 AA.
 AC Q949M4;
 DT 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
 DE Hypothetical protein At4g28760.
 GN Name=At4g28760;

Db 44 GLERILPQHQ 53

DR	InterPro; IPR01227; Ac transferase.
DR	InterPro; IPR02085; acyl_xn_family.
DR	InterPro; IPR01034; GroES_like.
DR	InterPro; IPR00794; Ketoacyl_synth.
DR	InterPro; IPR06163; Phosphateth_bind.
DR	InterPro; IPR06165; Ppantne_S.
DR	Pfam; PF00698; Acyl_transf_1.
DR	Pfam; PRO0107; ADH_Zinc_N.
DR	Pfam; PRO0109; Ketcacyl_synt.
DR	Pfam; PRO0201; Ketcacyl_synt_C.
DR	Pfam; PRO0550; PP-binding.
DR	PROSITE; PS50075; ACP_DOMAIN.
DR	PROSITE; PS00012; PHOSPHOPANTETHINE.
KW	SEQUENCE 2530 AA; 274185 MW; TBC2008E66BB8FF CRC64;
Query Match	Best Local Similarity 64.5%; Score 40; DB 2; Length 2530; Matches 8; Conservative 0; Pred. No. 3.5e+02; Indels 0; Gaps 0;
Oy	3 EALPRTHESQ 12
Db	1339 EALPRTHEQQ 1348
RESULT 17	PRELIMINARY; PRT; 248 AA.
Q8YXKG	PRELIMINARY; PRT; 248 AA.
ID	087XKG
AC	087XKG_ PRELIMINARY; PRT; 248 AA.
DT	01-JUN-2003 (Tremblrel. 24, Created)
DT	01-JUN-2003 (Tremblrel. 24, Last sequence update)
DT	01-MAR-2004 (Tremblrel. 26, Last annotation update)
DE	Amino acid ABC transporter, permease protein.
GN	OrderredlocusNames=SP01172;
OS	Pseudomonas syringae (pv tomato).
OC	Bacter; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC	Pseudomonadaceae; Pseudomonas.
OX	NCBI_TaxID=323;
RN	[1]
SEQUENCE FROM N.A.	
RC	STRAIN=D3000;
RX	MEDLINE=2834015; PubMed=12929499; DOI=10.1073/pnas.1731982100;
RA	Buell C.R., Jeardar V., Lindeberg M., Selengut J.T., Paulsen I.T., Gwin M.L., Dodson R.J., DeBoy R.T., Durkin A.S., Kolonay J.F., Madupu R., Daugherty S.C., Brinkac L.M., Beanan M.J., Haft D.H., Nelson W.C., Davidsen T.M., Zafar N., Zhou L., Liu J., Yuan Q., Khouri H.M., Fedorova N.B., Tran B., Russell D., Berry K.J., Utterback T.R., Van Aken S.E., Feldblyum T.V., D'Ascenzo M., Deng W.-L., Ramos J.R., Alfano J.R., Castainhour S., Chatterjee A.K., Delaney T.P., Lazarowitz S.G., Martin G.B., Schneider D.J., Tang X., Bender C.L., White O., Fraser C.M., Collier A.; "The complete genome sequence of the Arabidopsis and tomato pathogen Pseudomonas syringae pv. tomato D3000.", Proc. Natl. Acad. Sci. U.S.A. 100:1081-1086(2003).
CC	-- FUNCTION: Part of a binding-protein-dependent transport system. Probably responsible for the translocation of the substrate across the membrane (By similarity).
CC	-- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC	-- SIMILARITY: Belongs to the binding-protein-dependent transport system permease family.
DR	EMBL; AE016871; AA057628; 1.
DR	TIGR; PSPO412; -
DR	GO; GO:0016021; C: integral to membrane; IEA.
DR	GO; GO:0005215; F:transporter activity; IEA.
DR	INTERPRO; IPR000515; BPD_transp.
DR	INTERPRO; IPR01065; HEQ0 ABC_3TM.
DR	Pfam; PF00528; BPD_transp_I.
DR	TIGR3M; TIGR01726; HEQ0_pemt_3TM.
DR	PROSITE; PS50938; ABC_TML.
DR	Complete proteome; Transmembrane; Transport.
SQ	SEQUENCE 248 AA; 27601 MW; ADBB9778338279BD CRC64;
Query Match	Best Local Similarity 62.9%; Score 39; DB 2; Length 248; Matches 8; Conservative 1; Pred. No. 44; Indels 0; Gaps 0; Mismatches 2; R
Oy	1 GIEALPRTHES 11
Db	133 GIEALPKGOES 143
RESULT 18	PRELIMINARY; PRT; 271 AA.
Q9VAP7	PRELIMINARY; PRT; 271 AA.
ID	Q9VAP7
AC	Q9VAP7_ PRELIMINARY; PRT; 271 AA.
DT	01-MAY-2000 (Tremblrel. 13, Created)
DT	01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT	25-OCT-2004 (Tremblrel. 28, Last annotation update)
DE	CG17985_PA (ID36633p).
GN	ORFnames=CG17985;
OS	Drosophila melanogaster (Fruit fly).
OC	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydriidae; Drosophilidae; Drosophila.
OC	NCBI_TaxID=7227;
OX	[1]
RN	SEQUENCE FROM N.A.
RX	MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
RA	Adams M.D., Celinker S.E., Holt R.A., Evans J.D., Ammann D.P., Scherer S.E., Li P.W., Hoskins R.A., Gallo R.F., George R.A., Lewis S.B., Richards S., Ashburner M., Henderson S.N., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Brandon R.C., Rogers Y.H., Blazej R.G., Champe M., Peiffer B.D., Wan K.H., Doyle C., Baxter E.G., Heit G., Nelson C.R., Abril J.F., Abyzov A., An H.J., Andrews-Pfannkoch C., Baldwin D., Bailew R.M., Basu A., Baxendale J., Basyraktagrogli L., Bailey E.M., Beeben K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S., Bortkova D., Borckin M.R., Brottier P., Brottier P., Burris K.C., Busam D.A., Butler H., Cadieu B., Center A., Chandra I., Cherry J.M., Cawley S., Dahake C., Davenport L.B., Davies P., de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M., Dodson K., Douc L.B., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., Durbin K.J., Evangelista C.C., Ferraz C., Ferraria S., Fleischmann W., Foaler C., Gabril A.E., Garg N.S., Gelbart W.M., Glaser K., Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M., Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J., Hoskin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C., Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z., Labko P., Lei Y., Levitt A.C., Li J., Li Z., Liang Y., Lin X., Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D., Merkulov G., Milashina N.V., Mobarry C., Morris J., Mosherfi A., Mount S.M., Moy M., Murphy B., Murphy L., Muzy Y., Nelson D.M., Nelson D.R., Nelson K.A., Nusskern D.R., Paclet J.M., Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G., Reinert K., Renning K., Saunders R.D., Scheeler F., Shen H., Shue B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T., Spier E., Spradling A.C., Stapleton M., Strong R., Sun E., Svartek R., Tector C., Turner R., Venter E., Wang A.H., Wang X., Wang Z.Y., Wasserman D.A., Weinstock G.M., Weissenbach J., Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., Ye J., Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O., Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.; "The genome sequence of Drosophila melanogaster.", Science 287:2185-2195(2000).
RN	[2]
RX	MEDLINE=22426055; PubMed=12537568;
RA	Celinker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A., Patel S., Adams M., Champé M., Dugan S.P., Frise S., Hodgson A., George R.A., Hoskins R.A., Laverty T., Muzy N.D.M., Nelson C.R., Paclib J.M., Park S., Peiffer B.D., Richards S., Sodergren E.J., Svartek R., Tabor K., Staapelen M., Sutton G.G., Venter C., Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.,

RT "Finishing a whole-genome shotgun: Release 3 of the *Drosophila melanogaster* euchromatic genome sequence.";
 RN [3] Bio. / 3:RESEARCH0079-RESEARCH0079(2002).

SEQUENCE FROM N.A.

RT MEDLINE=22426070; PubMed=12537573;
 RA Kaminker J.S., Bergman C.M., Krommiller B., Carlson J., Svirskas R.,
 RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
 RA Ashburner M., Celinker S.E.;
 RT "The transposable elements of the *Drosophila melanogaster* euchromatin: a genomic perspective.";
 RL Genome Biol. 3:RESEARCH0084-RESEARCH0084 (2002).

[4]

RN SEQUENCE FROM N.A.

RX MEDLINE=22426069; PubMed=12537572;

RA Mira S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
 RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
 RA Smith C.D., Tupy J.L., Whitfield E.S.J., Bayraktaroglu L., Bernat B.P.,
 RA Bettencourt B.R., Celinker S.E., de Grey A.D., Drysdale R.A.,
 RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
 RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
 RA Lewis S.E., "Annotation of the *Drosophila melanogaster* genome: a systematic review";
 RT Genome Biol. 3:RESEARCH0083-RESEARCH0083 (2002).

[5]

RN SEQUENCE FROM N.A.

RG FlyBase;
 RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
 RN [6]

RN SEQUENCE FROM N.A.

RG FlyBase;
 RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
 RN [7]

RN SEQUENCE FROM N.A.

RC STRAIN=Berkeley;

RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
 RA Chamele M., Chavez C., Dorsett V., Farfán D., Frise E., George R.,
 RA Gonzalez M., Guarín H., Li P., Liao G., Mizanda A., Mungall C.J.,
 RA Nuncio J., Pacieb J., Paragas V., Park S., Phouanenavong S., Wan K.,
 RA Yu C., Lewis S.E., Rubin G.M., Celinker S.;
 RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL; AR003840; AAH59218.1; -;
 DR EMBL; AT051872; AAK93296.1; -;
 DR InterPro; Q9V4P7; -;
 DR FlyBase; FBgn0033199; CG17985;
 DR InterPro; IPR02482; LYM;
 DR Pfam; PF01476; LYSM_1;
 DR SMART; SM00257; LYSM_1;
 SQ SEQUENCE 271 AA; 30342 MW; 97EC5A4F937B2D60 CRC64;

Query Match 2 IEAPRTHESQ 12
 Best Local Similarity 72.7%; Pred. No. 51;
 Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 Db 272 IEALERBRHSQ 282

RESULT 20

Q6CKAO ID Q6CKAO PRELIMINARY; PRT; 294 AA.
 AC Q6CKAO;
 DT 25-OCT-2004 (TREMblrel. 28, Created)
 DT 25-OCT-2004 (TREMblrel. 28, Last sequence update)
 DT 25-OCT-2004 (TREMblrel. 28, Last annotation update)
 DE Similar to sp|P25605 Saccharomyces cerevisiae YCL009c ILV6
 DE acetolactate synthase;
 DE OS Kluyveromyces lactis NRRl Y-1140.
 OC Eukaryota; Fungi; Ascomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Kluyveromyces.
 OX NCBI_TAXID=670;
 RN [1]

RN SEQUENCE FROM N.A.

RC STRAIN=NRL Y-1140;

RG Genolvures;
 RA Dujon B., Sherman D., Fischer G., Durrens P., Casabrigola S.;
 RA Lafontaine I., de Montigny J., Marck C., Neveuville C., Talla B.,
 RA Gorffard N., Frangeul L., Agil M., Anthouard V., Babour A., Barbe V.,
 RA Barnay S., Bianchin S., Beckerich J.M., Beyne E., Bleijkaert C.,
 RA Boisrame A., Boyer J., Cattolico L., Confinolleti F., de Darvaru A.,
 RA Despont L., Fabre E., Fairhead C., Ferry-Dumazet H., Gropi A.,
 RA Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
 RA Kerrest A., Koszul R., Lemire M., Lésur T., Ma L., Müller H.,
 RA Niaud J.M., Nikolski M., Ortas S., Oriol-Kalogeropoulos O.,
 RA Pellez S., Potier S., Richard G.F., Straub M.U., Suleau A.,
 RA Swemme C., Tekata F., Wesołowski-Louvel M., Westhof E., Wirth B.,
 RA Zeniou-Meyer M., Zivanovic I., Bolotin-Fukuhara M., Thierry A.,
 RA Boucher C., Caudron B., Scarpelli C., Gaillardin C., Weissbach J.,
 RA Wincker P., Souillet J.L.;
 RT "Genome evolution in yeasts.";
 RL Nature 430:35-44 (2004).

RN [2]

RN SEQUENCE FROM N.A.

RC STRAIN=NRL Y-1140;

RA Genoscope;
 RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; CR8216; CAG98347.1; -;
 DR GO; GO:0003984; Facetolactate synthase activity; IEA.
 DR GO; GO:001597; F-amino acid binding; IEA.
 DR GO; GO:0009082; P-branched chain family amino acid biosynthesis; IEA.
 DR GO; GO:0008152; P:metabolism; IEA.

OS Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
 OC Vibionaceae; Vibrio.

Qy	1 GIEALPRTHESQ 12	Db	: 115
Db	142 GIEALARWHDPP 153		
RESULT 24			
ID Q86111	PRELIMINARY;	PRT;	400 AA.
AC Q86111;			
DT 01-JUN-2003 (TREMBrel. 24, Created)			
DT 01-JUN-2003 (TREMBrel. 24, Last sequence update)			
DT 01-MAR-2004 (TREMBrel. 26, Last annotation update)			
DE Hypothetical protein.			
OS Dictyostelium discoideum (Slime mold).			
OC Eukaryota; Mycetozoa; Dictyostellida; Dictyostelium.			
OX NCBI_TaxID=44689;			
RN [1]	SEQUENCE FROM N.A.		
RC STRAIN=X4;			
RX MEDLINE=22092622; PubMed=12097910; DOI=10.1038/nature00847;			
RA Gloeckner G., Eichinger L., Szafrański K., Pachabat J., Dear P.,			
RA Lehmann R., Baumgart C., Parra G., April J.F., Guigo R., Kumpf K.,			
RA Tunggal B., Cox E., Quail M.A., Platzer M., Rosenthal A., Noegel A.A.,			
RT "Sequence analysis of chromosome 2 of Dictyostellium discoideum.";			
RL Nature 418:79-85(2002).			
RN [2]	SEQUENCE FROM N.A.		
RC STRAIN=X4;			
RA Baumgart C.;	Submitted (ISB-P2003) to the EMBL/GenBank/DBJ databases.		
DR EMBL: AC117075; AA050797; 1.			
DR InterPro: IPR009457; DUBI1084.			
DR Pfam: PF06454; DUF1084; 1.			
KW Hypothetical protein.			
SQ SEQUENCE 400 AA; 45637 MW; F973507E054D3014 CRC64;			
Query Match Best Local Similarity 62.9%; Score 39; DB 2; Length 400; Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;			
Qy 2 IEALPRTHESQ 12			
Db 209 IFALPRTHESQ 219			
RESULT 25			
Q9IC82	PRELIMINARY;	PRT;	838 AA.
ID Q9IC82			
AC Q9IC82;			
DT 01-MAR-2001 (TREMBrel. 16, Created)			
DT 01-MAR-2001 (TREMBrel. 16, Last sequence update)			
DE Rb-associated protein.			
OS Homo sapiens (Human).			
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OX Primates; Catarrhini; Hominidae; Homo.			
RN [1]	SEQUENCE FROM N.A.		
RP MEDLINE=24040887; PubMed=10244455; DOI=10.1006/brcr.2000.3242;			
RA Wen H. Ao S.;			
RT "Rpp5, a novel leucine zipper protein, binds to the retinoblastoma protein.";			
RT protein.; Biochem. Biophys. Res. Commun. 275:141-148(2000).			
DR EML; AF122619; AUG13723.1; -.			
DR PIR; JCTJ363; JCTJ363.			
SEQUENCE 838 AA; 94780 MW; LC8D20BRA1038348 CRC64;			
Query Match Best Local Similarity 62.9%; Score 39; DB 2; Length 838; Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;			
Qy 2 IEALPRTHESQ 12			

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Gibbs R.A.,
 FAITEY J., Heaton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimes J.J., Myers R.M., Butterfield Y.S.,
 RA Krzwinbki M.I., Skalska U., Smailus D.E., Schnurch A., Schein J.E.,
 RA Jones S.J., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences"; Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RL [2]
 RN RP TISSUE=Skin;
 RC TISSUE=Uterus;
 RA Strausberg R.;
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RA Strausberg R.;
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
 CC -!- SIMILARITY: Contains 1 RING-type zinc finger.
 DR EMBL; BC018647; AAH18647_1; -;
 DR EMBL; BC006133; AAH06133_1; -;
 DR GO; GO:000151; C:ubiquitin ligase complex; IEA.
 DR GO; GO:0004842; F:ubiquitin-protein ligase activity; IEA.
 DR GO; GO:0008270; F:zinc ion binding; IEA.
 DR GO; GO:0016567; P:protein ubiquitination; IEA.
 DR InterPro; IPR01841; Znf_ring.
 DR Pfam; PF00097; zf-C3HC4_1.
 DR SMART; SN00184; RING_1; 1.
 PROSITE; PS55089; ZF_RING_2; 1.
 DR Metal-binding; Zinc; Zinc-finger.
 KW NON_TER 1
 SQ SEQUENCE 1030 AA; 113677 MW; 8F0985AA9F500A96 CRC64;
 Query Match 62.9%; Score 39; DB 2; Length 1030;
 Best Local Similarity 72.7%; Pred. No. 2.1e+02;
 Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 DE Hypothetical protein.
 GN ORFlames-Tb927.2-5740;
 OS Trypanosoma brucei.
 OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatida; Trypanosoma.
 RN NCBI_TaxID=5691;
 RP SEQUENCE FROM N.A.
 RX MEDLINE=>2789168; PubMed=12907728; DOI=10.1093/nar/gkg673;
 RA El-Sayed N.M.A., Ghedin E., Song J., MacLeod A., Brigaud F.,
 RA Larkin C., Wanless D., Peterson J., Hou L., Taylor S., Tweedie A.,
 RA Bitau N., Khaila G.H., Lin M., Mason T., Hannick L., Calier E.,
 RA Blandin G., Bartholomeu D., Simpson A.J., Kaul S., Zhao H., Pai G.,
 RA Van Aken S., Utterback T., Haas B., Koo H.L., Unayam L., Suh B.,
 RA Gerrard C., Leech V., Qi R., Zhou S., Schwartz D., Fieldblum T.,
 RA Salzberg S., Tait A., Turner M.R., Ulu E., White O., Melville S.,
 RA Adams M.D., Fraser C.M., Donelson J.E.; "The sequence and analysis of Trypanosoma brucei chromosome II.";
 RT Nucleic Acids Res. 31:856-4863(2003).
 RL EMBL; AE017170; AAQ16031_1; -.
 DR PRELIMINARY; PRT; 1030 AA.
 ID 075150; SQ TISSUE=Brain;
 DT 01-NOV-1998 (TREMBLrel. 08, Created)
 DT 01-NOV-1998 (TREMBLrel. 08, last sequence update)
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
 DE KIAA0661 protein (Fragment).
 GN NameKIAA0661,
 Homo sapiens (Human).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
 OC Mammalia; Buteraria; Primates; Catarhini; Hominidae; Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=>84403860; PubMed=9734911;
 RA Ishikawa K., Nagase T., Suyama M., Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.; "Prediction of the coding sequences of unidentified human genes. X. The complete sequences of 100 new cDNA clones from brain which can code for large proteins in vitro.;"
 RT code for large proteins in vitro.";

RESULT 28
 ID 075150; PRELIMINARY; PRT; 1030 AA.
 AC 075150;
 DT 01-NOV-1998 (TREMBLrel. 08, Created)
 DT 01-NOV-1998 (TREMBLrel. 08, last sequence update)
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
 DE KIAA0661 protein (Fragment).
 GN NameKIAA0661,
 Homo sapiens (Human).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
 OC Mammalia; Buteraria; Primates; Catarhini; Hominidae; Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=>84403860; PubMed=9734911;
 RA Ishikawa K., Nagase T., Suyama M., Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.; "Prediction of the coding sequences of unidentified human genes. X. The complete sequences of 100 new cDNA clones from brain which can code for large proteins in vitro.;"
 RT code for large proteins in vitro.";

RESULT 29
 ID 075150; PRELIMINARY; PRT; 127 AA.
 AC 075150;
 DT 01-OCT-2003 (TREMBLrel. 25, Created)
 DT 01-OCT-2003 (TREMBLrel. 25, Last sequence update)
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
 DE Hypothetical protein.
 GN ORFlames-Tb927.2-5740;
 OS Trypanosoma brucei.
 OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatida; Trypanosoma.
 RN NCBI_TaxID=5691;
 RP SEQUENCE FROM N.A.
 RX MEDLINE=>2789168; PubMed=12907728; DOI=10.1093/nar/gkg673;
 RA El-Sayed N.M.A., Ghedin E., Song J., MacLeod A., Brigaud F.,
 RA Larkin C., Wanless D., Peterson J., Hou L., Taylor S., Tweedie A.,
 RA Bitau N., Khaila G.H., Lin M., Mason T., Hannick L., Calier E.,
 RA Blandin G., Bartholomeu D., Simpson A.J., Kaul S., Zhao H., Pai G.,
 RA Van Aken S., Utterback T., Haas B., Koo H.L., Unayam L., Suh B.,
 RA Gerrard C., Leech V., Qi R., Zhou S., Schwartz D., Fieldblum T.,
 RA Salzberg S., Tait A., Turner M.R., Ulu E., White O., Melville S.,
 RA Adams M.D., Fraser C.M., Donelson J.E.; "The sequence and analysis of Trypanosoma brucei chromosome II.";
 RT Nucleic Acids Res. 31:856-4863(2003).
 RL EMBL; AE017170; AAQ16031_1; -.
 DR PRELIMINARY; PRT; 310 AA.
 ID 08C114; SQ TISSUE=Brain;
 AC 08C114;
 DT 01-MAR-2003 (TREMBLrel. 23, Created)
 DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
 DE BC023814 protein.

RESULT 30
 ID 08C114; PRELIMINARY; PRT; 310 AA.
 AC 08C114;
 DT 01-MAR-2003 (TREMBLrel. 23, Created)
 DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)

GN Name=BC023814;
 OS Mus musculus (Mouse);
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=FVB/N; TISSUE=Mammary tumor. C3;
 RX MEDLINE=22389257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Sherman C.M., Schuler G.D.,
 RA Ait schulz S.F., Zeeberg B., Buetow K.H., Schaeffer G.D.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Matsubara K., Farmer A.A., Rubin G.M., Hong L.,
 RA Diatchenko L., Matsubara K., Farmer A.A., Rubin G.M., Hong L.,
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Scheetz T.E.,
 RA Bromstein M.J., Usdin T.B., Toshiyuki S., Casavant T.L., Prange C.,
 RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Millahy S.J.,
 RA Borak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Soedergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Heitman E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Sherechenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smallius D.E., Schniech A., Schein J.E.,
 RA Jones S.J., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human
 RT cDNA sequences";
 RT and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=FVB/N; TISSUE=Mammary tumor. C3;
 RA Strausberg R.;
 RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC023814; AAH23814.1; -;
 DR MGII: MGII:2387197; BC02314;
 SQ SEQUENCE 310 AA; 34271 MW; 121D28A1B471A032 CRC64;
 Query Match 61.3%; Score 38; DB 2; Length 310;
 Best Local Similarity 50.0%; Pred. No. 88;
 Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
 Qy 1 GIEALPRTHE 10
 Qy 296 GVGQGIPRVE 305
 Db 296 GVGQGIPRVE 305

Search completed: August 1, 2005, 08:48:19
 Job time : 180 secs

OM protein - protein search, using sw model									
Run on:	Copyright (c) 1993 - 2005 Compugen Ltd.								
GenCore version 5.1.6									
Title:	US-10-663-74918	Search time 42 Seconds	29	34	54.8	700	4	US-09-2522-991A-0922-94	34
Perfect score:	62	1 GIBALPRTHESQ 12	30	31	54.8	1088	4	US-09-233-877-4	30
Sequence:	BLOSUM62		31	34	54.8	2504	4	US-09-949-016-6454	31
Scoring table:	Gapp 10.0 , Gapext 0.5		32	33	53.2	123	4	US-09-270-67-61706	32
Searched:	51345 seqs, 74649064 residues		33	33	53.2	162	4	US-10-067-433-18	33
Post-processing:	Minimum Match 0%		34	33	53.2	203	4	US-09-248-996A-6241	34
Maximum DB seq length:	200000000		35	33	53.2	241	4	US-09-217-5945-3	35
Post-processing:	Maximum Match 10%		36	33	53.2	273	4	US-09-252-991A-20798	36
Post-processing:	Listing first 150 summaries		37	33	53.2	283	4	US-09-270-767-46148	37
Total number of hits satisfying chosen parameters:	51345		38	33	53.2	295	4	US-09-252-991A-21169	38
Minimum DB seq length:	0		39	33	53.2	313	4	US-09-022-540-14667	39
Maximum DB seq length:	200000000		40	33	53.2	348	4	US-09-540-236-2479	40
Post-processing:	Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.		41	33	53.2	387	2	US-08-919-627-3	41
Database :	Issued_Patents_AA:*		42	33	53.2	387	3	US-09-095-245-3	42
	1: /cgn2_6/pctodata/1/iaa/5A_COMB_pep:*		43	33	53.2	364	4	US-09-438-046-13	43
	2: /cgn2_6/pctodata/1/iaa/5A_COMB_pep:*		44	33	53.2	386	4	US-09-533-092-1360	44
	3: /cgn2_6/pctodata/1/iaa/6B_COMB_pep:*		45	33	53.2	387	1	US-08-713-882-3	45
	4: /cgn2_6/pctodata/1/iaa/6B_COMB_pep:*		46	33	53.2	388	2	US-08-919-627-5	46
	5: /cgn2_6/pctodata/1/iaa/PCTUS_COMB_pep:*		47	33	53.2	387	2	US-08-919-279-552	47
	6: /cgn2_6/pctodata/1/iaa/backfiles1.pep:*		48	33	53.2	409	4	US-09-252-991A-31550	48
			49	33	53.2	428	4	US-09-543-683A-7693	49
			50	33	53.2	443	3	US-09-134-001C-3148	50
			51	33	53.2	473	4	US-09-270-767-37633	51
			52	33	53.2	473	4	US-09-270-767-52850	52
			53	33	53.2	519	4	US-08-956-171E-5230	53
			54	33	53.2	519	4	US-08-781-986A-5230	54
			55	33	53.2	536	4	US-09-902-500-13091	55
			56	33	53.2	570	4	US-09-248-766A-19123	56
			57	33	53.2	637	4	US-09-107-532A-5217	57
			58	33	53.2	637	4	US-08-842-079-6	58
			59	33	53.2	645	4	US-09-252-991A-23641	59
			60	33	53.2	671	3	US-08-912-079-17	60
			61	33	53.2	671	4	US-09-252-991A-16789	61
			62	33	53.2	699	3	US-09-638-857-6	62
			63	33	53.2	699	4	US-09-338-855-17	63
			64	33	53.2	700	3	US-09-15-127-8	64
			65	33	53.2	700	4	US-09-315-127-9	65
			66	33	53.2	700	4	US-09-252-991A-18848	66
			67	33	53.2	700	4	US-09-252-991A-20966	67
			68	33	53.2	700	4	US-09-270-767-36726	68
			69	33	53.2	700	4	US-09-270-767-51943	69
			70	33	53.2	700	4	US-09-270-767-51943	70
SUMMARIES									
Result No.	Score	Query Length	DB ID	Description	Sequence 11, Appl	Sequence 15, Appl	Sequence 4, Appl	Sequence 19260, A	Sequence 20411, A
1	62	100.0	237	2	US-08-578-709-11	Sequence 11, Appl	Sequence 15, Appl	Sequence 4, Appl	Sequence 19260, A
2	62	100.0	500	2	US-08-578-709-15	Sequence 11, Appl	Sequence 15, Appl	Sequence 4, Appl	Sequence 19260, A
3	40	64.5	2584	3	US-08-936-135.4	Sequence 11, Appl	Sequence 15, Appl	Sequence 4, Appl	Sequence 19260, A
4	37	59.7	201	4	US-09-232-991A-19360	Sequence 11, Appl	Sequence 15, Appl	Sequence 4, Appl	Sequence 19260, A
5	37	59.7	241	4	US-09-252-991A-0411	Sequence 11, Appl	Sequence 15, Appl	Sequence 4, Appl	Sequence 19260, A
6	37	59.7	257	4	US-09-270-767-42280	Sequence 11, Appl	Sequence 15, Appl	Sequence 4, Appl	Sequence 19260, A
7	37	59.7	392	4	US-09-902-540-13511	Sequence 11, Appl	Sequence 15, Appl	Sequence 4, Appl	Sequence 19260, A
8	37	59.7	568	4	US-09-499-039A-0669	Sequence 11, Appl	Sequence 15, Appl	Sequence 4, Appl	Sequence 19260, A
9	36	58.1	251	4	US-09-252-991A-21713	Sequence 11, Appl	Sequence 15, Appl	Sequence 4, Appl	Sequence 19260, A
10	36	58.1	507	3	US-08-860-633A-19	Sequence 11, Appl	Sequence 15, Appl	Sequence 4, Appl	Sequence 19260, A
11	36	58.1	507	3	US-09-81-476-19	Sequence 11, Appl	Sequence 15, Appl	Sequence 4, Appl	Sequence 19260, A
12	36	58.1	507	4	US-09-910-087-19	Sequence 11, Appl	Sequence 15, Appl	Sequence 4, Appl	Sequence 19260, A
13	36	58.1	509	3	US-08-860-633A-21	Sequence 11, Appl	Sequence 15, Appl	Sequence 4, Appl	Sequence 19260, A
14	36	58.1	509	3	US-09-81-475-21	Sequence 11, Appl	Sequence 15, Appl	Sequence 4, Appl	Sequence 19260, A
15	36	58.1	509	4	US-09-910-087-21	Sequence 11, Appl	Sequence 15, Appl	Sequence 4, Appl	Sequence 19260, A
16	58.1	509	4	US-09-940-016-5930	Sequence 11, Appl	Sequence 15, Appl	Sequence 4, Appl	Sequence 19260, A	Sequence 11, Appl
17	36	58.1	531	4	US-09-252-991A-22250	Sequence 11, Appl	Sequence 15, Appl	Sequence 4, Appl	Sequence 19260, A
18	36	58.1	556	4	US-09-940-016-9398	Sequence 11, Appl	Sequence 15, Appl	Sequence 4, Appl	Sequence 19260, A
19	35.5	65.5	65	4	US-09-252-991A-31569	Sequence 11, Appl	Sequence 15, Appl	Sequence 4, Appl	Sequence 19260, A
20	34	54.8	105	4	US-09-107-532A-5673	Sequence 11, Appl	Sequence 15, Appl	Sequence 4, Appl	Sequence 19260, A
21	34	54.8	146	4	US-09-252-991A-31369	Sequence 11, Appl	Sequence 15, Appl	Sequence 4, Appl	Sequence 19260, A
22	34	54.8	151	4	US-09-252-991A-22920	Sequence 11, Appl	Sequence 15, Appl	Sequence 4, Appl	Sequence 19260, A
23	34	54.8	151	4	US-09-252-991A-22250	Sequence 11, Appl	Sequence 15, Appl	Sequence 4, Appl	Sequence 19260, A
24	34	54.8	340	4	US-09-198-452A-362	Sequence 11, Appl	Sequence 15, Appl	Sequence 4, Appl	Sequence 19260, A
25	34	54.8	384	4	US-09-438-185A-347	Sequence 11, Appl	Sequence 15, Appl	Sequence 4, Appl	Sequence 19260, A
26	34	54.8	542	4	US-09-489-039A-9564	Sequence 11, Appl	Sequence 15, Appl	Sequence 4, Appl	Sequence 19260, A
27	34	54.8	676	4	US-09-949-016-7426	Sequence 11, Appl	Sequence 15, Appl	Sequence 4, Appl	Sequence 19260, A

101
 102 32 51.6 436 4 US-09-949-016-6527
 103 32 51.6 444 4 US-09-949-016-8779
 104 32 51.6 469 4 US-09-374-909-1
 105 32 51.6 472 4 US-09-489-039A-8418
 106 32 51.6 561 4 US-09-252-991A-31113
 107 32 51.6 564 4 US-09-252-991A-28765
 108 32 51.6 568 1 US-08-528-199-1
 109 32 51.6 612 2 US-08-746-283-31
 110 32 51.6 612 2 US-08-746-257A-29
 111 32 51.6 613 2 US-08-746-283-1
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 113 32 51.6 613 2 US-08-746-283-5
 114 32 51.6 613 2 US-08-746-257A-1
 115 32 51.6 613 3 US-08-746-283-48
 116 32 51.6 632 4 US-09-315-127-2
 117 32 51.6 632 4 US-09-315-127-3
 118 32 51.6 664 4 US-09-421-632-2
 119 32 51.6 665 4 US-09-309-572-14
 120 32 51.6 665 4 US-09-718-096-14
 121 32 51.6 694 3 US-08-252-991A-32382
 122 32 51.6 694 3 US-08-724-586-2
 123 32 51.6 694 4 US-09-421-632-2
 124 32 51.6 705 2 US-08-655-640-2
 125 32 51.6 708 2 US-08-655-640-4
 126 32 51.6 709 1 US-08-461-333-2
 127 32 51.6 709 3 US-08-464-167-2
 128 32 51.6 709 3 US-09-159-512-3
 129 32 51.6 709 3 US-08-476-798-2
 130 32 51.6 711 1 US-08-145-681-2
 131 32 51.6 711 1 US-08-154-019-4
 132 32 51.6 711 1 US-08-154-019-4
 133 32 51.6 711 1 US-08-154-019-4
 134 32 51.6 711 1 US-08-154-019-4
 135 32 51.6 711 1 US-08-461-333-4
 136 32 51.6 711 2 US-08-456-703-2
 137 32 51.6 711 2 US-08-456-106-2
 138 32 51.6 711 3 US-08-464-167-4
 139 32 51.6 711 3 US-08-464-167-4
 140 32 51.6 711 3 US-08-456-108-2
 141 32 51.6 711 3 US-08-476-798-4
 142 32 51.6 711 3 US-09-257-577-2
 143 32 51.6 711 4 US-09-633-739-2
 144 32 51.6 711 5 PCT-US93-03614-2
 145 32 51.6 722 4 US-09-902-540-10649
 146 32 51.6 740 1 US-08-309-512-10
 147 32 51.6 740 5 PCT-US92-08756A-10
 148 32 51.6 752 1 US-08-309-512-8
 149 32 51.6 752 5 PCT-US92-08756A-8
 150 32 51.6 765 1 US-08-309-512-5

RESULT 1
 Sequence 11, Application US/08578709
 Patent No. 5814509

GENERAL INFORMATION:

APPLICANT: TANABE, Tadashi

TITLE OF INVENTION: PROSTACYCLIN SYNTHASE DERIVED FROM HUMAN NUMBER OF SEQUENCES: 17

CORRESPONDENCE ADDRESS:

ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK & SEAS STREET: 2100 Pennsylvania Avenue, N.W.

CITY: Washington STATE: D.C.

ZIP: 20037 COUNTRY: USA

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patent In Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/578-709
 FILING DATE: 28-DEC-1995 CLASSIFICATION: 435

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/JP95/00838 FILING DATE: 27-APR-1995 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: JP 114316/1994 FILING DATE: 28-APR-1994 ATTORNEY/AGENT INFORMATION:
 NAME: Gubinsky, Louis REGISTRATION NUMBER: 24,835 REFERENCE/DOCKET NUMBER: Q40439 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202)293-7060 TELEFAX: (202)293-7060

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/578,709
FILING DATE: 28-DEC-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP95/00838
FILING DATE: 27-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 114316/1994
FILING DATE: 28-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Gubinsky, Louis
REGISTRATION NUMBER: 24,835
REFERENCE/DOCKET NUMBER: Q40439
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)293-7060
TELEFAX: (202)293-7060

ALIGNMENTS

INFORMATION FOR SEQ ID NO: 15:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 500 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein

RESULT 3
 Query Match 100.0%; Score 62; DB 2; Length 500;
 Best Local Similarity 100.0%; Pred. No. 0.0027; Matches 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GIEALPRTHESQ 12
 Db 182 GIEALPRTHESQ 193

US-08-578-709-15

Query Match 100.0%; Score 62; DB 2; Length 500;
 Best Local Similarity 100.0%; Pred. No. 0.0027; Matches 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GIEALPRTHESQ 12
 Db 182 GIEALPRTHESQ 193

RESULT 4
 Sequence 4, Application US/08936135
 Patent No. 6054293
 GENERAL INFORMATION:
 APPLICANT: Tessier-Lavigne, Marc
 APPLICANT: He, Zhigang
 APPLICANT: Chen, Hang
 TITLE OF INVENTION: Semaphorin Receptors
 NUMBER OF SEQUENCES: 26
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
 STREET: 75 DENISE DRIVE
 CITY: HILLSBOROUGH
 STATE: CALIFORNIA
 COUNTRY: USA
 ZIP: 94010

COMPUTER READABLE FORM:
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08936,135
 FILING DATE:
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: OSMAN, RICHARD A
 REFERENCE/DOCKET NUMBER: UG97-288-2
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (650) 343-4341
 TELEX/FAX: (650) 343-4342
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 2584 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide

RESULT 5
 Sequence 5, Application US/09252991A
 Patent No. 6551795
 GENERAL INFORMATION:
 APPLICANT: Marc J. Rubenfield et al.
 TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
 FILE REFERENCE: 107196.136
 CURRENT APPLICATION NUMBER: US/09/252,991A
 CURRENT FILING DATE: 1999-02-18
 PRIOR APPLICATION NUMBER: US 60/074,788
 PRIOR FILING DATE: 1998-02-18
 PRIOR APPLICATION NUMBER: US 60/094,190
 PRIOR FILING DATE: 1998-07-27
 NUMBER OF SEQ ID NOS: 33142
 SEQ ID NO 20411
 LENGTH: 241

RESULT 6
 Sequence 6, Application US/09270767
 Patent No. 6703491
 GENERAL INFORMATION:
 APPLICANT: Homburger et al.
 TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
 FILE REFERENCE: File Reference: 7326-094
 CURRENT APPLICATION NUMBER: US/09/270,767
 CURRENT FILING DATE: 1999-03-17
 NUMBER OF SEQ ID NOS: 62517
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO 42280
 LENGTH: 257

RESULT 7
 Sequence 7, Application US/09252991A
 Patent No. 6551795
 GENERAL INFORMATION:

US-09-270-767-42280

Query Match

59.7%; Score 37; DB 4; length 257;

Best Local Similarity 66.7%; Pred. No. 48;

Matches 6; Conservative 2; Mismatches 1;

Indels 0; Gaps 0;

SBQ ID NO 83 LEAIPRHE 91

RESULT 7

US-09-902-540-13511

Sequence 13511, Application US/09902540

Patent No. 6833447

GENERAL INFORMATION:

APPLICANT: Marc J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

FILE REFERENCE: 107196.136

CURRENT APPLICATION NUMBER: US/09/252, 991A

PRIORITY NUMBER: US 60/074, 788

PRIOR FILING DATE: 1998-02-18

PRIORITY APPLICATION NUMBER: US 60/094, 190

PRIORITY FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 21713

LENGTH: 251

TYPE: PRT

ORGANISM: Myxococcus xanthus

US-09-902-540-13511

Query Match

59.7%; Score 37; DB 4; Length 392;

Best Local Similarity 54.5%; Pred. No. 76;

Matches 6; Conservative 4; Mismatches 1;

Indels 0; Gaps 0;

SBQ ID NO 2 LEALPRTHESQ 12

Db 166 LQALRWHETR 176

RESULT 8

US-09-489-039A-10969

Sequence 10969, Application US/09489039A

Patent No. 6610836

GENERAL INFORMATION:

APPLICANT: Gary Breton et. al

TITLE OF INVENTION: NUCLEAR ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA

TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 2709_200401

CURRENT APPLICATION NUMBER: US/09/489, 039A

CURRENT FILING DATE: 2000-01-27

PRIOR APPLICATION NUMBER: US 60/117,747

PRIOR FILING DATE: 1999-01-29

NUMBER OF SEQ ID NOS: 14342

SBQ ID NO 10969

LENGTH: 568

TYPE: PRT

ORGANISM: Klebsiella pneumoniae

US-09-489-039A-10969

Query Match

59.7%; Score 37; DB 4; Length 568;

Best Local Similarity 58.3%; Pred. No. 1.1e+02;

Matches 7; Conservative 2; Mismatches 3; Indels 0;

Gaps 0;

SBQ ID NO 1 GIEALPRTHESQ 12

Db 422 GIEVVRRLHQSQ 433

Sequence 21713, Application US/09252991A
Patent No. 6551195
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252, 991A
PRIORITY NUMBER: US 60/074, 788
PRIOR FILING DATE: 1998-02-18
PRIORITY APPLICATION NUMBER: US 60/094, 190
PRIORITY FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 21713
LENGTH: 251TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-21713

Query Match

58.1%; Score 36; DB 4; Length 251;

Best Local Similarity 65.7%; Pred. No. 71;

Matches 6; Conservative 1; Mismatches 2;

Indels 0; Gaps 0;

SBQ ID NO 2 LEALPRTHESQ 10

Db 20 VEQAPRTH 28

RESULT 10

US-08-860-631A-19

Sequence 19, Application US/08860635A

Patent No. 6143878

GENERAL INFORMATION:

APPLICANT: Koopman, Peter

TITLE OF INVENTION: SOX-9 GENE AND PROTEIN AND

TITLE OF INVENTION: USE IN THE REGENERATION OF BONE OR CARTILAGE

NUMBER OF SEQUENCES: 21

CORRESPONDENCE ADDRESS:

ADDRESSEE: Scully, Scott, Murphy & Presser

STREET: 400 Garden City Plaza

CITY: Garden City

STATE: NY

COUNTRY: U. S. A.

ZIP: 11530

COMPUTER READABLE FORM:

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSEQ Version 1.5

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/860, 635A

FILING DATE: 29-MAY-1997

CLASSIFICATION: 514

PRIORITY APPLICATION DATA:

APPLICATION NUMBER: AU PM9714

FILING DATE: 29-NOV-1994

APPLICATION NUMBER: AU PM9835

FILING DATE: 05-DEC-1994

APPLICATION NUMBER: PCT/AU95/00799

FILING DATE: 29-NOV-1995

ATTORNEY/AGENT INFORMATION:

NAME: DiGilio, Frank S.

REGISTRATION NUMBER: 31,346

REFERENCE/DOCKET NUMBER: 10981

TELECOMMUNICATION INFORMATION:

TELEPHONE: 516-742-4343

TELEFAX: 516-742-4366

TELEX:

INFORMATION FOR SEQ ID NO: 19:

SEQUENCE CHARACTERISTICS:

LENGTH: 507 amino acids

RESULT 9

US-09-252-991A-21713

RESULT 11
 Query Match 58.1%; Score 36; DB 3; Length 507;
 Best Local Similarity 41.7%; Pred. No. 1.5e+02;
 Matches 5; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
 Strandedness: single
 Topology: linear
 Molecule Type:
 US-08-660-635A-19

Qy 1 GIEALPRTTHSQ 12
 Db 483 GVPSPQTHSPQ 494

RESULT 11
 Sequence 19, Application US/09281476
 Pattern No. 6316397

GENERAL INFORMATION:
 APPLICANT: Koopman, Peter
 APPLICANT: Goodfellow, Peter
 TITLE OF INVENTION: SOX-9 GENE AND PROTEIN AND USE IN THE REGENERATION OF BONE OR CARTILAGE
 TITLE OF INVENTION: USE IN THE REGENERATION OF BONE OR CARTILAGE
 NUMBER OF SEQUENCES: 21
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Scully, Scott, Murphy & Presser
 STREET: 400 Garden City Plaza
 CITY: Garden City
 STATE: NY
 COUNTRY: U.S.A.
 ZIP: 11530

COMPUTER READABLE FORM:
 COMPUTER TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FastSEQ Version 1.5

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/910,087
 FILING DATE: 20-JUL-2001
 CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: AU PM9714
 FILING DATE: 29-NOV-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: DIGILO, Frank S.
 REGISTRATION NUMBER: 31,346
 REFERENCE/DOCKET NUMBER: 10981
 FILING DATE: 05-DEC-1994
 APPLICATION NUMBER: PCT/AU95/00799
 TELEPHONE: 516-742-4343
 TELEFAX: 516-742-4366
 TELEX: <Unknown>

INFORMATION FOR SEQ ID NO: 19:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 507 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 MOLECULE TYPE: <Unknown>
 SEQUENCE DESCRIPTION: SEQ ID NO: 19:
 US-09-910-087-19

Query Match 58.1%; Score 36; DB 4; Length 507;
 Best Local Similarity 41.7%; Pred. No. 1.5e+02;
 Matches 5; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
 Strandedness: single
 Topology: linear
 Molecule Type:
 US-09-281-476-19

RESULT 13
 Query Match 58.1%; Score 36; DB 3; Length 507;
 Best Local Similarity 41.7%; Pred. No. 1.5e+02;
 Matches 5; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
 Strandedness: single
 Topology: linear
 Molecule Type:
 US-08-860-635A-21

Qy 1 GIEALPRTTHSQ 12
 Db 483 GVPSPQTHSPQ 494

RESULT 12
 Sequence 19, Application US/09910087
 Patent No. 673413

GENERAL INFORMATION:
 APPLICANT: Koopman, Peter
 APPLICANT: Goodfellow, Peter
 TITLE OF INVENTION: SOX-9 GENE AND PROTEIN AND USE IN THE REGENERATION OF BONE OR CARTILAGE
 TITLE OF INVENTION: USE IN THE REGENERATION OF BONE OR CARTILAGE
 NUMBER OF SEQUENCES: 21
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Scully, Scott, Murphy & Presser
 STREET: 400 Garden City Plaza
 CITY: Garden City
 STATE: NY
 COUNTRY: U.S.A.
 ZIP: 11530

COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FastSEQ Version 1.5

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/910,087
 FILING DATE: 20-JUL-2001
 CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: AU PM9714
 FILING DATE: 29-NOV-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: DIGILO, Frank S.
 REGISTRATION NUMBER: 31,346
 REFERENCE/DOCKET NUMBER: 10981
 FILING DATE: 05-DEC-1994
 APPLICATION NUMBER: PCT/AU95/00799
 TELEPHONE: 516-742-4343
 TELEFAX: 516-742-4366
 TELEX: <Unknown>

INFORMATION FOR SEQ ID NO: 19:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 507 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 MOLECULE TYPE: <Unknown>
 SEQUENCE DESCRIPTION: SEQ ID NO: 19:
 US-09-910-087-19

Query Match 58.1%; Score 36; DB 4; Length 507;
 Best Local Similarity 41.7%; Pred. No. 1.5e+02;
 Matches 5; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
 Strandedness: single
 Topology: linear
 Molecule Type:
 US-09-910-087-19

RESULT 13
 Query Match 58.1%; Score 36; DB 3; Length 507;
 Best Local Similarity 41.7%; Pred. No. 1.5e+02;
 Matches 5; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
 Strandedness: single
 Topology: linear
 Molecule Type:
 US-08-860-635A-21

Qy 1 GIEALPRTTHSQ 12
 Db 483 GVPSPQTHSPQ 494

RESULT 13
 Query Match 58.1%; Score 36; DB 3; Length 507;
 Best Local Similarity 41.7%; Pred. No. 1.5e+02;
 Matches 5; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
 Strandedness: single
 Topology: linear
 Molecule Type:
 US-08-860-635A-21

Qy 1 GIEALPRTTHSQ 12
 Db 483 GVPSPQTHSPQ 494

STREET: 400 Garden City Plaza
 CITY: Garden City
 STATE: NY
 COUNTY: U.S.A.
 ZIP: 11530
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FastSEQ Version 1.5
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/860 635A
 FILING DATE: 29-MAY-1997
 CLASSIFICATION: 514
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: AU PM9714
 FILING DATE: 29-NOV-1994
 APPLICATION NUMBER: AU PM9835
 FILING DATE: 05-DEC-1994
 APPLICATION NUMBER: PCT/AU95/00799
 ATTORNEY/AGENT INFORMATION:
 NAME: DIGIGLIO, Frank S.
 REGISTRATION NUMBER: 31,346
 REFERENCE/DOCKET NUMBER: 10981
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 516-742-4343
 TELEX:
 TELEFAX: 516-742-4366
 INFORMATION FOR SEQ ID NO: 21:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 509 amino acids
 STRANDEDNESS: Single
 TOPOLOGY: Linear
 MOLECULE TYPE: protein
 US-09-281-476-21

Query Match 58.1%; Score 36; DB 3; Length 509;
 Best Local Similarity 41.7%; Pred. No. 1.5e+02; Matches 5; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
 QY 1 GIEALPRTHESQ 12
 Db 485 GPVSIPQTHSPQ 496

RESULT 14
 US-09-281-476-21
 Sequence 21, Application US/09281476
 Patent No. 6316597
 GENERAL INFORMATION:
 APPLICANT: Koopman, Peter
 APPLICANT: Goodfellow, Peter
 TITLE OF INVENTION: SOX-9 GENE AND PROTEIN AND USE IN THE REGENERATION OF BONE OR CARTILAGE
 NUMBER OF SEQUENCES: 21
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Scully, Scott, Murphy & Presser
 STREET: 400 Garden City Plaza
 CITY: Garden City
 STATE: NY
 COUNTRY: U.S.A.
 ZIP: 11530
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/910,087
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: AU PM9714
 FILING DATE: 29-NOV-1994
 APPLICATION NUMBER: AU PM9835
 FILING DATE: 05-DEC-1994
 APPLICATION NUMBER: PCT/AU95/00799
 FILING DATE: 29-NOV-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: DIGIGLIO, Frank S.
 REGISTRATION NUMBER: 31,346
 REFERENCE/DOCKET NUMBER: 10981
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 516-742-4343
 TELEX:
 TELEFAX: 516-742-4366
 INFORMATION FOR SEQ ID NO: 21:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 509 amino acids
 STRANDEDNESS: Single
 TOPOLOGY: Linear
 MOLECULE TYPE: protein
 US-09-281-476-21

RESULT 15
 US-09-910-087-21
 Sequence 21, Application US/09910087
 Patent No. 6737413
 GENERAL INFORMATION:
 APPLICANT: Koopman, Peter
 APPLICANT: Goodfellow, Peter
 TITLE OF INVENTION: SOX-9 GENE AND PROTEIN AND USE IN THE REGENERATION OF BONE OR CARTILAGE
 NUMBER OF SEQUENCES: 21
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Scully, Scott, Murphy & Presser
 STREET: 400 Garden City Plaza
 CITY: Garden City
 STATE: NY
 COUNTRY: U.S.A.
 ZIP: 11530
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/910,087
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: AU PM9714
 FILING DATE: 29-NOV-1994
 APPLICATION NUMBER: AU PM9835
 FILING DATE: 05-DEC-1994
 APPLICATION NUMBER: PCT/AU95/00799
 FILING DATE: 29-NOV-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: DIGIGLIO, Frank S.
 REGISTRATION NUMBER: 31,346
 REFERENCE/DOCKET NUMBER: 10981
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 516-742-4343
 TELEX:
 TELEFAX: 516-742-4366

TELEX: <unknown>
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 509 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 21:
US-09-910-087-21

Query Match 58.1%; Score 36; DB 4; Length 509;
Best Local Similarity 41.7%; Pred. No. 1.6e+02; Length 531;
Matches 5; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GIEALPRTHSQ 12
Db 485 GPVPSIPOTHSPQ 496

RESULT 16
US-09-949-016-5930
Sequence 5930, Application US/09949016
PATENT NO. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-03-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 5930
LENGTH: 509
TYPE: PRT
ORGANISM: Human
US-09-949-016-5930

Query Match 58.1%; Score 36; DB 4; Length 509;
Best Local Similarity 41.7%; Pred. No. 1.5e+02; Length 531;
Matches 5; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GIEALPRTHSQ 12
Db 485 GPVPSIPOTHSPQ 496

RESULT 17
US-09-252-991A-26690
Sequence 26690, Application US/09252991A
PATENT NO. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEAR ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 31569
LENGTH: 65
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-31569

Query Match 56.5%; Score 35; DB 4; Length 65;
Best Local Similarity 63.6%; Pred. No. 25; Length 65;
Matches 7; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GIEALPRTHS 11
Db 471 GIELPLPRT 478

RESULT 18
US-09-949-016-9398
Sequence 9398, Application US/09949016
PATENT NO. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 9398
LENGTH: 556
TYPE: PRT
ORGANISM: Human
US-09-949-016-9398

Query Match 58.1%; Score 36; DB 4; Length 556;
Best Local Similarity 41.7%; Pred. No. 1.7e+02; Length 531;
Matches 5; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GIEALPRTHSQ 12
Db 532 GPVPSIPOTHSPQ 543

RESULT 19
US-09-252-991A-31569
Sequence 31569, Application US/09252991A
PATENT NO. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEAR ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 31569
LENGTH: 65
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-31569

Query Match 56.5%; Score 35; DB 4; Length 65;
Best Local Similarity 63.6%; Pred. No. 25; Length 65;
Matches 7; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GIEALPRTHS 11
Db 471 GIELPLPRT 478

Db 11 | GAPRPRTHRS 21

RESULT 20
 sequence 6573, Application US/09107532A
 Patent No. 658325
 GENERAL INFORMATION:
 APPLICANT: Lynn A Doucette-Stamm and David Bush
 TITLE OF INVENTION: NUCLEAR ACID AND AMINO ACID SEQUENCES RELATING TO
 NUMBER OF SEQUENCES: 7310
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: GENOME THERAPEUTICS CORPORATION
 STREET: 100 Beaver Street
 CITY: Waltham
 STATE: Massachusetts
 COUNTRY: USA
 ZIP: 02454
 COMPUTER READABLE FORM:
 MEDIUM TYPE: CD/ROM ISO9660
 COMPUTER: PC
 OPERATING SYSTEM: <Unknown>
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/107,532A
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: 60/085,598
 FILING DATE: 30-Jun-1998
 APPLICATION NUMBER: 60/051571
 FILING DATE: July 2, 1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Arinello, Pamela Deneke
 REGISTRATION NUMBER: 40,489
 REFERENCE/DOCKET NUMBER: GTC-012
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (781)893-5007
 TELEFAX: (781)893-8277
 INFORMATION FOR SEQ ID NO: 6573:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 105 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 HYPOTHETICAL: YES
 ORIGINAL SOURCE:
 ORGANISM: Enterococcus faecium
 FEATURE:
 NAME/KEY: misc_feature
 LOCATION: (B) LOCATION 1...105
 /- SEQUENCE DESCRIPTION: SEQ ID NO: 6573:
 US-09-107-532A-6573

Query Match 54.8%; Score 34; DB 4; Length 105;
 Best Local Similarity 58.3%; Pred. No. 65;
 Matches 7; Conservative 1; Mismatches 4;
 QY 1 GIEALPRTHESQ 12
 Db 52 GIPFLDPROHPSR 63

RESULT 21
 Query Match 54.8%; Score 34; DB 4; Length 105;
 Best Local Similarity 58.3%; Pred. No. 65;
 Matches 7; Conservative 1; Mismatches 4;
 Indels 0; Gaps 0;
 US-09-252-991A-31369

; Sequence 31369, Application US/09252991A
 ; Patent No. 6551795
 ; GENERAL INFORMATION:
 ; APPLICANT: Marc J. Rubenfield et al.
 ; TITLE OF INVENTION: NUCLEAR ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
 ; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
 ; FILE REFERENCE: 107196_136
 ; CURRENT APPLICATION NUMBER: US/09/252,991A
 ; CURRENT FILING DATE: 1999-03-18
 ; PRIOR APPLICATION NUMBER: US 60/074,788
 ; PRIOR FILING DATE: 1998-02-18
 ; PRIOR APPLICATION NUMBER: US 60/094,190
 ; PRIOR FILING DATE: 1998-07-27
 ; NUMBER OF SEQ ID NOS: 33142
 ; SEQ ID NO 31369
 ; LENGTH: 146
 ; TYPE: PRT
 ; ORGANISM: Pseudomonas aeruginosa
 US-09-252-991A-31369

Query Match 54.8%; Score 34; DB 4; Length 146;
 Best Local Similarity 50.0%; Pred. No. 92;
 Matches 6; Conservative 3; Mismatches 3;
 Indels 0; Gaps 0;
 QY 1 GIEALPRTHESQ 12
 Db 38 GAEAVPQBEKR 49

RESULT 22
 Sequence 22920, Application US/09252991A
 Patent No. 6551795
 GENERAL INFORMATION:
 APPLICANT: Marc J. Rubenfield et al.
 TITLE OF INVENTION: NUCLEAR ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
 FILE REFERENCE: 107196_136
 CURRENT APPLICATION NUMBER: US/09/252,991A
 CURRENT FILING DATE: 1999-03-18
 PRIOR APPLICATION NUMBER: US 60/074,788
 PRIOR FILING DATE: 1998-02-18
 PRIOR APPLICATION NUMBER: US 60/094,190
 PRIOR FILING DATE: 1998-07-27
 NUMBER OF SEQ ID NOS: 33142
 SEQ ID NO 22920
 LENGTH: 151
 TYPE: RT
 ORGANISM: Pseudomonas aeruginosa
 US-09-252-991A-22920

Query Match 54.8%; Score 34; DB 4; Length 151;
 Best Local Similarity 50.0%; Pred. No. 96;
 Matches 6; Conservative 2; Mismatches 4;
 Indels 0; Gaps 0;
 QY 1 GIEALPRTHESQ 12
 Db 129 GLLOLPRIPHGQ 140

RESULT 23
 Sequence 22250, Application US/09252991A
 Patent No. 6551795
 GENERAL INFORMATION:
 APPLICANT: Marc J. Rubenfield et al.
 TITLE OF INVENTION: NUCLEAR ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
 TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
 FILE REFERENCE: 107196_136
 CURRENT APPLICATION NUMBER: US/09/252,991A
 CURRENT FILING DATE: 1999-03-18
 PRIOR APPLICATION NUMBER: US 60/074,788
 PRIOR FILING DATE: 1998-02-18
 PRIOR APPLICATION NUMBER: US 60/094,190
 PRIOR FILING DATE: 1998-07-27
 NUMBER OF SEQ ID NOS: 33142
 SEQ ID NO 22250
 LENGTH: 303
 TYPE: PRT
 ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-22250

Db 105 GIEALPAILES 115

Query Match 54.8%; Score 34; DB 4; Length 303;

Best Local Similarity 75.0%; Pred. No. 2e+02; Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 TEALPRTH 9
Db 138 VEALPRGH 145

RESULT 24

US-09-198-452A-362
Sequence 362, Application US/09198452A
Patent No. 6559294

GENERAL INFORMATION:

APPLICANT: Griffais, R.

TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments

TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, preve

FILE REFERENCE: 9710_003_999
TITLE OF INVENTION: FILE REFERENCE: 9710_003_999

TITLE OF INVENTION: and treatment of infection

CURRENT APPLICATION NUMBER: US/09/198,452A

NUMBER OF SEQ ID NOS: 6849

SEQ ID NO 362

LENGTH: 340

TYPE: PRT

ORGANISM: Chlamydia pneumoniae

US-09-198-452A-362

Query Match 54.8%; Score 34; DB 4; Length 340;

Best Local Similarity 72.7%; Pred. No. 2.3e+02; Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GIEALPAILES 11
Db 61 GIEALPAILES 71

RESULT 25

US-09-439-185A-347
Sequence 347, Application US/09439185A
Patent No. 6822071

GENERAL INFORMATION:

APPLICANT: Stephens, Richard

APPLICANT: Mitchell, Wayne

APPLICANT: Kalman, Sue

APPLICANT: Davis, Ronald

APPLICANT: The Regents of the University of California

TITLE OF INVENTION: Chlamydia Pneumoniae Genome Sequence

FILE REFERENCE: 018941-00411US

CURRENT APPLICATION NUMBER: US/09/438,185A

CURRENT FILING DATE: 2002-03-13

PRIOR APPLICATION NUMBER: US 60/108,279

PRIOR FILING DATE: 1998-11-12

PRIOR APPLICATION NUMBER: US 60/128,606

PRIOR FILING DATE: 1999-04-08

SOFTWARE: FastSBO for Windows Version 3.0

SEQ ID NO 347

LENGTH: 384

TYPE: PRT

ORGANISM: Chlamydia pneumoniae

FEATURE: OTHER INFORMATION: CPPn0345

US-09-438-185A-347

Query Match 54.8%; Score 34; DB 4; Length 384;
Best Local Similarity 72.7%; Pred. No. 2.6e+02; Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;Qy 1 GIBAURRTHES 11
Db ||||| 11RESULT 26
US-09-439-039A-9564
Sequence 9564, Application US/09489039A
Patent No. 6610336

GENERAL INFORMATION:

APPLICANT: Gary Breton et. al

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA

FILE REFERENCE: 2709_2004001
CURRENT APPLICATION NUMBER: US/09/489,039A

CURRENT FILING DATE: 2000-01-27

PRIOR APPLICATION NUMBER: US 60/117,747

PRIOR FILING DATE: 1999-01-29

NUMBER OF SEQ ID NOS: 14342

SEQ ID NO 9564

LENGTH: 542

TYPE: PRT

ORGANISM: Klebsiella pneumoniae

US-09-489-039A-9564

Query Match 54.8%; Score 34; DB 4; Length 542;

Best Local Similarity 66.7%; Pred. No. 3.8e+02; Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 4 ALPRTHESQ 12
Db 511 ALPRTHNGK 519RESULT 27
US-09-949-016-7426
Sequence 7426, Application US/09949016
Patent No. 681239

GENERAL INFORMATION:

APPLICANT: Venter, J. Craig et al.

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: C001307

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-20

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR FILING DATE: 2000-10-03

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FastSBO for Windows Version 4.0

SEQ ID NO 7426

LENGTH: 676

TYPE: PRT

ORGANISM: Human

US-09-949-016-7426

Query Match 54.8%; Score 34; DB 4; Length 676;
Best Local Similarity 75.0%; Pred. No. 4.8e+02; Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;Qy 5 LPRTHESQ 12
Db 424 LPRPHEAQ 431RESULT 28
US-09-252-991A-29072Sequence 29072, Application US/09252991A
Patent No. 6551755

GENERAL INFORMATION:

APPLICANT: Marc J. Rubenfield et al.

TITLE OF INVENTION: NUCLEAR ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

```

; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196..36
; CURRENT APPLICATION NUMBER: US/09/252,991A.
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO: 29072
; LENGTH: 700
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-29072

Query Match      54.8%; Score 34; DB 4; Length 700;
Best Local Similarity 60.0%; Pred. No. 5e+02; 2; Mismatches 6; Conservatve 2; Indels 0; Gaps 0;
Matches 6; Conservatve 2; Indels 0; Gaps 0;

Qy          2 LEALPRTHES 11
Db          213 LEAVPDAHES 222

RESULT 29
US-09-538-092-84
; Sequence 84, Application US/09538092
; Patent No. 675314
; GENERAL INFORMATION:
; APPLICANT: Giot, Loic
; APPLICANT: Mansfield, Traci A.
; TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
; FILE REFERENCE: 15966-542
; CURRENT APPLICATION NUMBER: US/09/538,092
; CURRENT FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 60/127,352
; PRIOR FILING DATE: 1999-04-01
; PRIOR APPLICATION NUMBER: 60/178,965
; PRIOR FILING DATE: 2000-02-01
; NUMBER OF SEQ ID NOS: 1387
; SOFTWARE: CuraPatSeqFormatter Version 0.9
; SBQ ID NO 84
; LENGTH: 1065
; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (0)..(0)
; OTHER INFORMATION: Polypeptide Accession Number YCR067C
US-09-538-092-84

Query Match      54.8%; Score 34; DB 4; Length 1065;
Best Local Similarity 50.0%; Pred. No. 7.8e+02; 2; Mismatches 5; Conservatve 3; Indels 0; Gaps 0;
Matches 5; Conservatve 3; Indels 0; Gaps 0;

Qy          2 LEALPRTHES 11
Db          296 VOLVPRVHES 305

RESULT 30
US-09-233-857-4
; Sequence 4, Application US/09233857
; Patent No. 649553
; GENERAL INFORMATION:
; APPLICANT: Flomman, Gregory
; APPLICANT: Flanagan, Peter
; TITLE OF INVENTION: HUMAN ORTHOLOGUES OF WART
; FILE REFERENCE: 239/251
; CURRENT APPLICATION NUMBER: US/09/233,857
; CURRENT FILING DATE: 1999-01-20
; EARLIER APPLICATION NUMBER: US/98 60/072,023
; EARLIER FILING DATE: 1998-01-21

; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSEQ For Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 1088
; TYPE: PRT
; ORGANISM: HUMAN
US-09-233-857-4
; Query Match      54.8%; Score 34; DB 4; Length 1088;
; Best Local Similarity 66.7%; Pred. No. 8e+02; 2; Mismatches 1; Conservatve 1; Indels 0; Gaps 0;
; Matches 6; Conservatve 1; Indels 0; Gaps 0;

Qy          1 GIEALPRTH 9
Db          385 GLEAPPRAH 393

Search completed: August 1, 2005, 08:49:47
Job time : 44 secs

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GenCore version 5.1.6
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Om protein - protein search, using sw model

Run on: August 1, 2005, 08:25:53 ; Search time 164 Seconds

(without alignments)
28.300 Million cell updates/sec

Title: US-10-663-749-18

Perfect score: 62

Sequence: 1 GIEALPRTHSQ 12

Scoring table: BLOSUM62

Gpop 10.0 , Gapext: 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters:

2105692

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 150 summaries

Database : A_Geneseq_16Dec04,*

1: geneseq1980s:*

2: geneseq1990s:*

3: geneseq2000s:*

4: geneseq2001s:*

5: geneseq2002s:*

6: geneseq2003ab:*

7: geneseq2004ab:*

8: geneseq2004b:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Score	Query	%	Match Length	DB ID	Description
1	62	100.0	237	2	ARR84562	Aarr84562 Human pro
2	62	100.0	500	2	ARR84561	Aarr84561 Human pro
3	62	100.0	500	7	ABD70342	Abd0342 Prostacyc
4	62	100.0	500	8	ADJ7121	Adj7121 Human mal
5	40	64.5	739	8	ADP64397	Adp64397 Trichoder
6	39	62.9	147	4	AAU50860	Aau50860 Propionib
7	39	62.9	147	6	ABR71779	Abm71779 Propionib
8	39	62.9	271	4	ABR66595	Abb66595 Drosophil
9	39	62.9	420	4	AAU63605	Aau63605 Propionib
10	39	62.9	420	4	ABM60124	Abm60124 Propionib
11	39	63.9	948	8	ADJ37227	Adj7227 Human nuc
12	38	61.3	509	4	ABR11798	Abbr11798 Human Gf
13	38	61.3	765	8	ADP64400	Adp64400 Trichoder
14	37	59.7	201	7	ABO70514	Abot70514 Pseudomon
15	37	59.7	241	7	ABO71665	Abot71665 Pseudomon
16	37	59.7	307	4	ABR58234	Abb58234 Drosophil
17	37	59.7	410	6	ABO00565	Abot00565 Novel hum
18	37	59.7	568	7	ABR64452	Abbr64452 Klabstall
19	36	58.1	568	5	ABP41544	Abp41544 Human ova
20	35	58.1	152	6	ABM69852	Abm69852 Photobacter
21	36	58.1	152	6	ABM69781	Abm69781 Photobacter
22	36	58.1	179	8	AKD16367	Adk16367 Nanoarcha
23	36	58.1	198	4	ADM40723	Adm40723 Human pol
24	36	58.1	251	7	ABO72967	Abot72967 Pseudomon
25	36	58.1	336	6	ABU21788	Abu21788 Protein e
98	34					

99	34	54.8	327	8	ABM83538	Abm83538 Human dia	FT	Peptide	1.. 237	/note= "prostacyclin-synthase (AA 1-237)"
100	34	54.8	327	8	ABM83542	Abm83542 Human dia	FT			
101	34	54.8	327	8	ABM83543	Abm83543 Human dia	XX			
102	34	54.8	327	8	ABM83537	Abm83537 Human dia	PN			
103	34	54.8	327	8	ABM83541	Abm83541 Human dia	XX			
104	34	54.8	327	8	ABM83539	Abm83539 Human dia	PD		09-NOV-1995.	
105	34	54.8	334	8	ADS2951	Adb26951 Bacterial	XX			
106	34	54.8	334	8	ADS2309	Adb27309 Bacterial	PF		27-APR-1995;	95MO-JP000838.
107	34	54.8	340	8	AYA4944	Ayv34944 Chlamydia	XX			
108	34	54.8	340	8	ADS2576	Adb26575 Bacterial	PR		28-APR-1994;	94JP-00114316.
109	34	54.8	342	4	ABG6560	Abg6560 Novel hum	XX			
110	34	54.8	357	2	ABR3440	Aar33440 Ornithine	PA	(TANAKA) TANABE T.		
111	34	54.8	371	4	ABG15569	Abg15569 Novel hum	XX			
112	34	54.8	397	6	ABM77496	Abm72496 Staphyloc	PT	Tanabe T;		
113	34	54.8	399	4	AMW8818	Aam8818 Human pro	XX			
114	34	54.8	399	7	ADL14196	Adl14196 Human src	DR			
115	34	54.8	399	8	ADS88194	Adb88194 Human pro	XX			
116	34	54.8	409	6	ABU23374	Abu233374 Protein e	XX			
117	34	54.8	421	6	ABU3666	Abu33666 Protein e	XX			
118	34	54.8	439	4	AMW9802	Aam9802 Human pro	PT			
119	34	54.8	445	4	AUW2626	Aau42626 Propionib	XX			
120	34	54.8	445	6	ABM3145	Abm3145 Propionib	XX			
121	34	54.8	459	3	AYA4413	Aay4413 Neisseria	PS			
122	34	54.8	489	7	ABD0367	Abd0367 Human nov	XX			
123	34	54.8	542	7	ABO63047	Abo63047 Klebsiell	CC			
124	34	54.8	548	8	ADM9983	Adm0983 Human pro	CC			
125	34	54.8	561	4	AAG67032	Aae67032 Human end	CC			
126	34	54.8	587	6	ABR53423	Abx53423 Protein s	CC			
127	34	54.8	587	7	ADK64684	Adk4684 Disease	CC			
128	34	54.8	628	8	ADS4965	Adz4965 Bacterial	CC			
129	34	54.8	637	7	ADP70478	Adt70478 Orphan re	XX			
130	34	54.8	679	4	ABB64462	Abb4462 Drosophil	CC			
131	34	54.8	700	7	ABO8326	Abp80326 Pseudomon	CC			
132	34	54.8	708	2	AAR71037	Aar71037 Draculin-	CC			
133	34	54.8	991	8	ABM8419	Abm8419 Human dia	CC			
134	34	54.8	1045	3	AGG38809	Aag38809 Arabidops	CC			
135	34	54.8	1045	6	AAE37151	Aaa37151 Drosophil	CC			
136	34	54.8	1046	8	ADH05550	Adh05550 Human nos	CC			
137	34	54.8	1046	8	ADQ8952	Adb8952 Antigens	CC			
138	34	54.8	1066	3	AAG38808	Aae39808 Arabidops	CC			
139	34	54.8	1087	4	ARG78992	Aag78992 Human can	CC			
140	34	54.8	1088	2	AYA0527	Aay0527 Human war	CC			
141	34	54.8	1088	3	ABD07663	Abd07663 Amino aci	CC			
142	34	54.8	1088	3	ABD07664	Abd07664 Amino aci	CC			
143	34	54.8	1109	7	ADP54494	Adt54494 Human nov	CC			
144	34	54.8	1125	7	ADC77580	Adc37580 Human nuc	CC			
145	34	54.8	1165	7	ADE07744	Ade07744 Novel pro	CC			
146	34	54.8	1256	3	AGG38807	Aag39807 Arabidops	CC			
147	34	54.8	2404	2	AAW3640	Aaw30640 HIV-1-NC7	DT			
148	34	54.8	2504	5	ABP5923	Abp54923 Human fat	XX			
149	34	54.8	5155	8	ADN7145	Adn31145 Thale cre	DE			
150	33	53.2	31	4	AAM20450	Aam20450 Peptide #	XX			

ALIGNMENTS

RESULT 1

XX											
DE											
XX											
XX											
XX											

RESULT 1
 AAR84562 ID AAR84562 standard; protein; 237 AA.
 AC AAR84562;
 XX DT 13-APR-1996 (first entry)
 XX DE Human prostacyclin-synthase partial sequence.
 XX KW Clone PHPGIS36; prostacyclin-synthase; Prostaglandin I2;
 KW circulatory disease; therapeutic; diagnosis; gene therapy.
 XX OS Homo sapiens.
 XX PH Key Location/Qualifiers

Key 1
 Peptide 1.. 237
 /note= "clone PHPGIS36 (see AAR84562)"
 Peptide 225.. 285
 /note= "clone phage lambda hPGIS141 (see AAR84564)"
 Peptide 226.. 500
 /note= "clone PHPGIS135 (see AAR84563)"

W0953013-A1.
 09-NOV-1995.
 27-APR-1995; 95MO-JP000838.
 28-APR-1994; 94JP-00114316.

PA (TANAKA) TANABE T.
 XX
 PI Tanabe T;
 XX
 DR WPI; 1995-393084/50.
 XX N-PSDB; AAT05316.
 XX Human prostacyclin synthase and DNA encoding it - useful in the investigation and treatment of diseases characterised by reduced prostaglandin I2 production.
 XX
 PS Claim 1; Page 46-48; 71pp; Japanese.
 CC Prostacyclin-synthase is produced by recombinant DNA methods and is used in patients to increase prostaglandin I2 (PGI2) production to treat diseases characterized by reduced PGI2 levels or by an imbalance between PGI2 and thromboxane A2 levels, such as circulatory diseases (thrombosis, angina pectoris, arteriosclerosis, myocardial infarction). The protein is also used in disease diagnosis
 XX
 SQ Sequence 500 AA;

Query Match	100.0%	Score	62;	DB	2;	Length	500;
Best Local Similarity	100.0%	Pred.	No.	0.007;	0;	Indels	0;
Matches	12;	Conservative	0;	Mismatches	0;	Gaps	0;

QY 1 GIEALPRTHSQ 12
 DB 182 GIEALPRTHSQ 193

RESULT 3

ID ADB70342 standard; protein; 500 AA.
 AC ADB70342;
 DT 04-DEC-2003 (first entry)
 DE Prostacyclin synthase SEQ ID NO:34.
 DB
 XX cancer; malignant pleural mesothelioma; MMP; lung adenocarcinoma; squamous carcinoma; medulloblastoma; prostate cancer; breast cancer; diffuse large B-cell lymphoma; follicular lymphoma; ovarian cancer; human; enzyme.
 KW
 OS Homo sapiens.
 XX
 PN WO2003021229-A2.
 XX
 PR 13-MAR-2003.
 PD
 XX
 PP 05-SEP-2002; 2002WO-US028203.
 PR 05-SEP-2001; 2001US-0317389P.
 PR 30-AUG-2002; 2002US-00236031.
 PR
 PA (BGHM) BRIGHAM & WOMENS HOSPITAL INC.
 XX
 PI Gordon GJ, Jensen RV, Gullans SR, Bueno R;
 XX
 PT WPI; 2003-29023/28.
 DR
 XX
 PT Diagnosing cancer cells in tissue sample, or determining prognosis or outcome of cancer patient, by calculating ratio of expression levels of genes that are differentially expressed in cancer and non cancer tissues.
 XX
 PS Claim 77; Page 154-156; 396pp; English.
 XX
 CC The present invention describes a method (M1) for diagnosing the presence of cancer cells or non-cancer cells in a tissue sample, or determining the prognosis or outcome of a cancer patient. M1 involves providing a set of genes differentially expressed in the prognosis or outcome of a cancer patient. M1 involves providing a set of genes that are differentially expressed in cancerous or non-cancerous conditions, determining the expression levels of the set of genes and calculating a ratio of the expression levels of the differentially expressed genes. M1 is useful for diagnosing the presence of cancer cells or non-cancer cells in a tissue sample, where the cancer is malignant pleural mesothelioma (MPM), lung adenocarcinoma, squamous carcinoma, medulloblastoma, prostate cancer, breast cancer, diffuse large B-cell lymphoma, follicular lymphoma and ovarian cancer, and for determining prognosis or outcome of a cancer patient. The ratio of expression levels of differentially expressed genes is used as an indicator of cancer type, cancer class, and/or cancer prognosis, all of which are useful for determining a course of treatment of a patient. The present sequence represents a human protein which is used in an example from the present invention.
 CC
 SQ Sequence 500 AA;

Query Match	100.0%	Score	62;	DB	7;	Length	500;
Best Local Similarity	100.0%	Pred.	No.	0.007;	0;	Indels	0;
Matches	12;	Conservative	0;	Mismatches	0;	Gaps	0;

QY 1 GIEALPRTHESQ 12
 DB 182 GIEALPRTHESQ 193

RESULT 4

ID ADJ37121 standard; protein; 500 AA.
 AC ADJ37121;
 DT 22-APR-2004 (first entry)
 DE Human malignant pleural mesothelioma (MPM) protein #13.
 DB
 XX Human; malignant pleural mesothelioma; MMP; tumour; lung adenocarcinoma; squamous carcinoma; medulloblastoma; prostate cancer; breast cancer; diffuse large B-cell lymphoma; follicular lymphoma; ovarian cancer; cyostatic.
 KW
 OS Homo sapiens.
 XX
 PN US2003219760-A1.
 XX
 PD 27-NOV-2003.
 XX
 PP 05-SEP-2002; 2002US-00236031.
 XX
 PR 05-SEP-2001; 2001US-0317389P.
 PR 30-AUG-2002; 2002US-0407431P.
 PR
 PA (BGHM) BRIGHAM & WOMENS HOSPITAL INC.
 XX
 PI Gordon GJ, Jensen RV, Gullans SR, Bueno R;
 XX
 PT WPI; 2004-141744/14.
 DR
 XX
 PT Diagnosing the presence of cancer or non-cancer cells in tissue sample, useful for diagnosing malignant pleural mesothelioma comprises determining ratio of expression level of a set of genes expressed in cancer tissues.
 XX
 PS Claim 77; SEQ ID NO 34; 53pp; English.
 XX
 CC The invention relates to a method of diagnosing the presence of cancer cells or non-cancer cells in a tissue sample, determining prognosis or outcome of a cancer patient, selecting a course of treatment for a subject having or suspected of having malignant pleural mesothelioma (MPM) and evaluating treatment of MPM comprising determining the ratio of the expression level of a set of genes differentially expressed in a cancer tissue. The cancer is chosen from MPM, lung adenocarcinoma,

CC squamous carcinoma; medulloblastoma; prostate cancer; breast cancer;
 CC diffuse large B-cell lymphoma; follicular lymphoma and ovarian cancer.
 CC The method is useful for diagnosing MPM in a subject suspected of having
 MPM which involves obtaining a tissue sample suspected of being cancerous
 from a subject and determining the expression of nucleic acid markers or
 its expression products in the tissue sample. This sequence represents a
 human MPM protein of the invention. Note: The sequence data for this
 patent did not form part of the printed specification but was obtained in
 electronic format directly from USPTO at seqdata.uspto.gov/sequence.html.

SQ Sequence 500 AA;

Query Match	100.0%	Score	62	DB	8	Length	500
Best Local Similarity	100.0%	Pred. No.	0.007	Indels	0	Mismatches	0
Matches	12	Gaps	0				

QY 1 GIEALPRTHESQ 12

Db 182 GIEALPRTHESQ 193

RESULT 5

ID ADP64397

ADP64397 standard; protein; 739 AA.

XX

AC ADP64397;

XX

DT 12-AUG-2004 (first entry)

XX

DB Trichoderma reesei beta-glucosidase BGL7 mature protein.

XX

KW Beta-glucosidase; BGL7; yeast dough; baked food; detergent; aroma; wine;

KW cellulase; biomass; bio-ethanol; enzyme; EC 3.2.1.21.

XX

OS Hypocrea jecorina.

XX

FH Key Location/Qualifiers

Misc-difference 7 /note= "Encoded by ATA codon of the sequences {seqid:1} and {seqid:4}"

Misc-difference 27 /note= "Encoded by GGC codon of the sequence {seqid:1}"

Misc-difference 61 /note= "Encoded by CT codon of the sequence {seqid:1}"

Misc-difference 66 /note= "Encoded by GCC codon of the sequence {seqid:1}"

Misc-difference 152 /note= "Encoded by MC codon of the sequence {seqid:1} and AAG codon of the sequence {seqid:4}"

Misc-difference 182 /note= "Encoded by TC codon of the sequence {seqid:1}"

Misc-difference 193 /note= "Encoded by ATG codon of the sequence {seqid:4}"

Misc-difference 240 /note= "Encoded by TC codon of the sequence {seqid:1}"

Misc-difference 249 /note= "Encoded by TC codon of the sequence {seqid:4}"

Misc-difference 265 /note= "Encoded by GGC codon of the sequence {seqid:1}"

Misc-difference 376 /note= "Encoded by GGC codon of the sequence {seqid:4}"

Misc-difference 382 /note= "Encoded by TAG codon of the sequence {seqid:1}"

Misc-difference 401 /note= "Encoded by GGC codon of the sequence {seqid:1}"

Misc-difference 437 /note= "Encoded by GGT codon of the sequence {seqid:1}"

Misc-difference 473 /note= "Encoded by CGG codon of the sequence {seqid:1}"

Misc-difference 474 /note= "Encoded by TTCATCAAT codons of the sequences {seqid:1} and {seqid:4}"

Misc-difference 490 /note= "Encoded by UT codon of the sequence {seqid:4}"

Misc-difference 556 /note= "Encoded by UT codon of the sequence {seqid:4}"

FT Misc-difference /notes= "Encoded by AA codon of the sequence {seqid:1}"

FT Misc-difference 594 /note= "Encoded by GRC codon of the sequence {seqid:4}"

FT Misc-difference 679 /note= "Encoded by GSC codon of the sequence {seqid:4}"

FT Misc-difference 682 /note= "Encoded by AUG codon of the sequence {seqid:1}"

FT Misc-difference 715 /note= "Encoded by TT codon of the sequence {seqid:1}"

FT Misc-difference 729 /note= "Encoded by GSC codon of the sequence {seqid:4}"

FT US2004102619-A1.

PR XX

DR XX

PR XX

PA (DUNN/) DUNN-COLEMAN N.

PA (WARD/) WARD M.

PI Dunn-Coleman N, Ward M;

XX

DR N-PSDB; ADP64396, ADP64399.

XX

PT Novel BGL7 polypeptide having beta glucosidase activity useful for improving yeast dough or baked good made from such dough, for preparing detergent compositions or for enhancing potential aroma finished wine product.

PT

PS Claim 18; SEQ ID NO 2; 25pp; English.

XX

CC The invention relates to beta-glucosidase BGL7 (EC 3.2.1.21) polypeptide and poly nucleotide from Trichoderma. The enzyme is useful for improving the characteristics of a yeast dough or baked good made from such dough, for preparing detergent composition, for enhancing the potential aroma of finished wine product, for hydrolysis of cellulose to its sugar components, for preparing cellulase composition for use in detergents or for degradation of biomass into sugar, for bioethanol production. The present sequence is Trichoderma reesei beta-glucosidase BGL7 mature protein.

CC

SQ Sequence 739 AA;

Query Match	64.5%	Score	40	DB	8	Length	739
Best Local Similarity	58.3%	Pred. No.	1.4e+02	Indels	0	Mismatches	4
Matches	7	Gaps	0				

QY 1 GIEALPRTHESQ 12

Db 3 GVSOLPSTHESQ 14

RESULT 6

ID AAU50660

AAU50660 standard; protein; 147 AA.

XX

AC AAU50660;

XX

DT 27-FEB-2002 (first entry)

XX

DE Propionibacterium acnes immunogenic protein #11556.

XX

SAPRO syndrome; synovitis; acne; pustulosis; hypertrichosis; osteomyelitis; uveitis; endophthalmitis; bone; joint; central nervous system; ELISA; inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay; dermatological; osteopathic; neuroprotectant.

XX

OS Propionibacterium acnes.

PN WO200181581-A2.
 XX
 PD 01-NOV-2001.
 XX
 PR 20-APR-2001; 2001WO-US012865.
 XX
 PR 21-APR-2000; 2000US-0199047P.
 PR 02-JUN-2000; 2000US-0208841P.
 PR 07-JUL-2000; 2000US-0216747P.
 XX
 PA (CORI-) CORIXA CORP.
 XX
 PI Skeiky YAW, Persing DH, Mitcham JL, Wang SS, Bhatia A;
 PT L'maisonneuve J, Zhang Y, Jen S, Carter D;
 XX DR WPI; 2001-611674/71.
 PT Propionibacterium acnes polypeptides and nucleic acids useful for
 PT vaccinating against and diagnosing infections, especially useful for
 PT treating acne vulgaris.
 XX Example 1; SEQ ID NO 11855; 1069PP; English.
 CC Sequences AAU39105-AAU6017 represent Propionibacterium acnes immunogenic
 CC polypeptides. The proteins and their associated DNA sequences are used in
 CC the treatment, prevention and diagnosis of medical conditions caused by
 CC P. acnes. The disorders include SAPHO syndrome (synovitis, acne,
 CC pustulosis, hyperosisis and osteomyelitis), uveitis and endophthalmitis.
 CC P. acnes is also involved in infections of bone, joints and the central
 CC nervous system, however it is particularly involved in the inflammatory
 CC lesions associated with acne vulgaris. A method for detecting the
 CC presence or absence of P. acnes in a patient comprises contacting a
 CC sample with a binding agent that binds to the proteins of the invention
 CC and determining the amount of bound protein in the sample. The
 CC polypeptides may be used as antigens in the production of antibodies
 CC specific for P. acnes protein. These antibodies can be used to
 CC downregulate expression and activity of P. acnes polypeptides and
 CC therefore treat P. acnes infections. The antibodies may also be used as
 CC diagnostic agents for determining P. acnes presence, for example, by
 CC enzyme linked immunosorbent assay (ELISA). Note: The sequence data for
 CC this patent did not form part of the printed specification, but was
 CC obtained in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX SQ Sequence 147 AA:
 Query Match 62.9%; Score 39; DB 4; Length 147;
 Best Local Similarity 70.0%; Pred. No. 38;
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 2 IEALPRTHES 11
 Db 129 IEQIPRTHRS 138
 RESULT 7
 ABM7179 Standard; protein; 147 AA.
 AC ABM47179;
 XX DT 20-OCT-2003 (first entry)
 XX DR Propionibacterium acnes predicted ORF-encoded polypeptide #11855.
 XX KW Acne vulgaris; antifiborrhoeic; dermatological; antibacterial;
 KW immunostimulant; immune response; vaccine.
 OS Propionibacterium acnes.
 XX PN WO2003033515-A1.
 XX
 PD 24-APR-2003.
 XX PR 11-OCT-2002; 2002WO-US03277.
 XX PR 15-OCT-2001; 2001US-00978825.
 XX PA (CORI-) CORIXA CORP.
 XX PI Mitcham JL, Skeiky YAW, Persing DH, Bhatia A, Maisonneuve JL;
 PT Zhang Y, Wang S, Jen S, Lodes MJ, Benson DR, Jones R, Carter D;
 PT Barth B, Vailleve-Douglas J;
 XX DR WPI; 2003-381789/36.
 XX PT New Propionibacterium acnes polypeptides and polynucleotides encoding the
 PT polypeptide, useful for diagnosing, preventing or treating acne vulgaris,
 PT or for stimulating an immune response specific for a P. acnes protein.
 XX PS Example 1; SEQ ID NO 11855; 1481PP; English.
 CC The invention relates to an isolated polynucleotide (ACF64435-ACF64733)
 CC encoding a Propionibacterium acnes protein. The invention also relates to
 CC polypeptides encoded by the polynucleotides (AKM35624-ABM64536) and to
 CC immunogenic fragments of P. acnes polypeptides. The invention
 CC additionally encompasses expression vectors and host cells comprising a
 CC polynucleotide of the invention; antibodies against polypeptides of the invention; a
 CC invention; fusion proteins comprising a polypeptide of the invention; a
 CC method for stimulating an immune response specific for a P. acnes
 CC polypeptide and an isolated T cell population comprising T cells prepared
 CC via this method; a vaccine composition (comprising P. acnes polypeptides,
 CC polynucleotides, antibodies, fusion proteins, T cell populations, or
 CC antigen-presenting cells that express the polypeptide); a method and kit
 CC for detecting or determining the presence or absence of P. acnes in a
 CC patient; and a method for inhibiting the development of P. acnes in a
 CC patient. The P. acnes polypeptides, polynucleotides, antibodies, fusion
 CC proteins, T cell populations or antigen-presenting cells that express the
 CC polypeptides are useful for diagnosing, preventing or treating acne
 CC vulgaris, or for stimulating an immune response specific for a P. acnes
 CC protein. The polynucleotides can also be used as probes or primers for
 CC nucleic acid hybridisation. The vaccine composition is useful for the
 CC stimulation of an immune response against P. acnes, or for treating acne,
 CC and the kit is useful for performing a diagnostic assay. The present
 CC sequence represents a polypeptide predicted to be encoded by an ORF (open
 CC reading frame) contained within the P. acnes polynucleotides of the
 CC invention. Note: The sequence data for this patent did not form part of
 CC the printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
 XX SQ Sequence 147 AA;
 Query Match 62.9%; Score 39; DB 6; Length 147;
 Best Local Similarity 70.0%; Pred. No. 38;
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 2 IEALPRTHES 11
 Db 129 IEQIPRTHRS 138
 RESULT 8
 ABM66595
 ID ABB66595 Standard; protein; 271 AA.
 XX AC ABB66595;
 XX AC ABB66595;
 XX DT 26-MAR-2002 (first entry)
 XX DE Drosophila melanogaster polypeptide SEQ ID NO 26577.
 XX KW Drosophila; developmental biology; cell signalling; insecticide;
 KW pharmaceutical.

OS Drosophila melanogaster.
 XX
 PN WO200171042-A2.
 XX
 PD 27-SEP-2001.
 XX
 PR 23-MAR-2001; 2001WO-US009231.
 XX
 PR 23-MAR-2000; 2000US-0191637P.
 PT 11-JUL-2000; 2000US-00614150.
 PT
 XX
 PA (PEKE) PE CORP NY.
 XX
 PI Venter JC, Adams M, Li PWD, Myers EW;
 XX
 DR WPI; 2001-656860/75.
 DR N-PSDB; ABL10698.
 XX
 PT New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell interactions.
 XX
 PT Disclosure; SEQ ID NO 26577; 21pp + Sequence Listing; English.
 CC
 CC The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL01840-ABL6175) and the encoded proteins (ABR57737-ABG2072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
 XX
 Sequence 271 AA;
 SQ
 Query Match 62.9%; Score 39; DB 4; Length 271;
 Best Local Similarity 63.6%; Pred. No. 73; Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 OQ 1 GIEALPRTHES 11
 Db 114 GLEALPAVHRS 124
 RESULT 9
 AAU3605
 ID AAU63605 standard; protein; 420 AA.
 XX
 AC AAU63605;
 XX
 DT 27-FEB-2002 (first entry)
 XX
 DE Propionibacterium acnes immunogenic protein #24501.
 XX
 KW SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis; uveitis; endophthalmitis; bone; joint; central nervous system; ELISA; inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay; dermatological; osteopathic; neuroprotectant.
 XX
 OS Propionibacterium acnes.
 XX
 WO200181581-A2.
 XX
 PD 01-NOV-2001.
 XX
 PR 20-APR-2001; 2001WO-US012865.
 XX
 PR 21-APR-2000; 2000US-0193047P.
 PR 02-JUN-2000; 2000US-0208841P.
 PR 07-JUL-2000; 2000US-0216747P.
 XX
 PA (CORI-) CORIXA CORP.
 XX
 PI Skeiky YAW, Persing DH, Mitcham JL, Wang SS, Bhatia A; L'maisonneuve J, Jen S, Carter D;
 XX
 DR WPI; 2001-616774/71.
 DR N-PSDB; AAS59634.
 XX
 PT Propionibacterium acnes polypeptides and nucleic acids useful for vaccinating against and diagnosing infections, especially useful for treating acne vulgaris.
 XX
 PS Claim 3; SEQ ID NO 24800; 1069pp; English.
 XX
 Sequences AAU9105-AAU68017 represent Propionibacterium acnes immunogenic polypeptides. The proteins and their associated DNA sequences are used in the treatment, prevention and diagnosis of medical conditions caused by P. acnes. The disorders include SAPHO syndrome (synovitis, acne, pustulosis, hypertriosis and osteomyelitis), uveitis and endophthalmitis. P. acnes is also involved in infections of bone, joints and the central nervous system, however it is particularly involved in the inflammatory lesions associated with acne vulgaris. A method for detecting the presence or absence of P. acnes in a patient comprises contacting a sample with a binding agent that binds to the proteins of the invention and determining the amount of bound protein in the sample. The polypeptides may be used as antigens in the production of antibodies specific for P. acnes proteins. These antibodies can be used to downregulate expression and activity of P. acnes polypeptides and therefore treat acne infections. The antibodies may also be used as diagnostic agents for determining P. acnes presence, for example, by enzyme linked immunosorbent assay (ELISA). Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
 XX
 Sequence 420 AA;
 SQ
 Query Match 62.9%; Score 39; DB 4; Length 420;
 Best Local Similarity 70.0%; Pred. No. 1.2e+02; Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 OQ 3 EALPRTHESQ 12
 Db 404 KAVPFRHESQ 413
 RESULT 10
 ABM60124
 ID ABM60124 standard; protein; 420 AA.
 XX
 AC ABM60124;
 XX
 DT 20-OCT-2003 (first entry)
 XX
 DE Propionibacterium acnes membrane-related polypeptide #24800.
 XX
 KW Acne vulgaris; antiseborrhoeic; dermatological; antibacterial; immunostimulant; immune response; vaccine.
 XX
 OS Propionibacterium acnes.
 XX
 WO2003033515-A1.
 XX
 PD 24-APR-2003.
 XX
 PR 11-OCT-2002; 2002WO-US012727.
 XX
 PR 15-OCT-2001; 2001US-00978825.
 XX
 PA (CORI-) CORIXA CORP.
 XX
 PI Mitcham JL, Skeiky YAW, Persing DH, Bhatia A, Maisonneuve JL; Zhang Y, Wang S, Jen S, Lodes MJ, Benson DR, Jones R, Carter D;

PI Barth B, Vailleve-Douglass J;
 XX WPI; 2003-381789/36.
 DR N-PSDB; ACF64563.
 XX
 PT New Propionibacterium acnes polypeptides and polynucleotides encoding the
 PT polypeptide, useful for diagnosing, preventing or treating acne vulgaris,
 PT or for stimulating an immune response specific for a P. acnes protein.
 XX
 PS Claim 3d; SEQ ID NO 24800; 1481pp; English.
 XX
 The invention relates to an isolated polynucleotide (ACF64435, ACF64733),
 CC encoding a Propionibacterium acnes protein. The invention also relates to
 CC polypeptides encoded by the Polynucleotides (ABM13524, ABM4536) and to
 CC immunogenic fragments of P. acnes polypeptides. The invention
 CC additionally encompasses expression vectors and host cells comprising a
 CC polynucleotide of the invention; antibodies against polypeptides of the
 CC invention; fusion proteins comprising a polypeptide of the invention; a
 CC method for stimulating an immune response specific for a P. acnes
 CC polypeptide and an isolated T cell population comprising T cells prepared
 via this method; a vaccine composition (comprising P. acnes polypeptides,
 CC polynucleotides, antibodies, fusion proteins, T cell populations, or
 CC antigen presenting cells that express the polypeptide); a method and kit
 for detecting or determining the presence or absence of P. acnes in a
 CC patient; and a method for inhibiting the development of P. acnes in a
 CC patient. The P. acnes polypeptides, polynucleotides, antibodies, fusion
 CC proteins, T cell populations or antigen-presenting cells that express the
 CC polypeptides are useful for diagnosing, preventing or treating acne
 vulgaris, or for stimulating an immune response specific for a P. acnes
 CC protein. The polynucleotides can also be used as probes or primers for
 CC nucleic acid hybridization. The vaccine composition is useful for the
 CC stimulation of an immune response against P. acnes, or for treating acne,
 CC and the kit is useful for performing a diagnostic assay. The present
 CC sequence represents a specifically claimed polypeptide which is predicted
 CC to be encoded by an ORF (open reading frame) contained within the P.
 CC acnes polynucleotides of the invention. Note: The sequence data for this
 CC patent did not form part of the printed specification, but was obtained
 CC in electronic format directly from WIPO at
 CC ftp://wipo.int/pub/published_pct_sequences
 XX
 Sequence 420 AA:
 Query Match 62.9%; Score 39; DB 6; Length 420;
 Best Local Similarity 70.0%; Pred. No. 1.2e+02;
 Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 Qy 3 BALPRTHESO 12
 Db 404 KAVPRRHESQ 413
 RESULT 11
 ID ADJ37227 standard; protein; 948 AA.
 XX
 AC ADJ37227;
 XX
 DT 22-APR-2004 (first entry)
 XX
 DE Human nucleic-acid associated protein NAAp-16 SEQ ID NO:16.
 XX
 KW human; nucleic-acid associated protein; NAAp-16; NAAp; antiparkinsonian;
 KW nootropic; neuroprotective; muscular; neuroleptic; antidiabetic;
 KW antithyroid; cytostatic; dermatological; antiinflammatory;
 KW immunosuppressive; anti-allergic; nephrotoxic; virostatic; antibacterial;
 KW fungicide; antiparasitic; protozoacide; antihelminthic;
 KW antarteriosclerotic; cardiovascular; gastrointestinal; hepatotropic;
 KW gene therapy; neurodegenerative disorder; Parkinson's disease; catatonia;
 KW Alzheimer's disease; muscular disorder; myotonic dystrophy; catatonia;
 KW endocrine disorder; diabetes; Grave's disease; cancer; leukemia;
 KW cervical cancer; breast cancer; immunological disorder; scleroderma;
 KW systemic lupus erythematosus; allergy; gastrointestinal disorder;
 KW Crohn's disease; renal disorder; Goodpasture's syndrome; infection;

KW cardiovascular disorder; atherosclerosis; hepatic diseases; cirrhosis.
 XX Homo sapiens.
 XX
 PN WO2004011604-A2.
 XX PD 05-FEB-2004.
 XX PR 23-JUL-2003; 2003WO-US023245.
 XX PR 26-JUL-2002; 2002US-0398907P.
 PR 30-AUG-2002; 2002US-044139P.
 PR 05-NOV-2002; 2002US-044094P.
 PR 17-JAN-2003; 2003US-0440912P.
 PR 24-JAN-2003; 2003US-0442419P.
 XX PA (INCY) INCYTE CORP.
 XX
 PI Mason PM, Swarnakar A, Jiang X, Jackson AA, Kable AE, Tang YT;
 PI Forsythe LJ, Elliott VS, Lee SY, Lee EA, Ison CH, Hatalia AJA;
 PI Khare R, Marquis JP, Bechta SD, Bullock SA, Blake JJ, Gandhi AR;
 PI Griffin JA, Lee S, Yue H, Yang YG, Sprague WW, Baughn MR, Wang JT;
 PI Gera M, Gietzen KJ, Nguyen DB, Lu DAM;
 XX DR ADJ37262.
 XX N-PSDB; ADJ37262.
 XX
 PT New nucleic acid-associated proteins (NAAp) polypeptides, useful for
 PT diagnosing, preventing and treating disorders with abnormal activity of
 PT NAAp, e.g. neurological, immunological, cardiovascular disorders and
 PT cancer.
 XX
 PS Claim 1; SEQ ID NO 16; 290pp; English.
 XX
 The present sequence represents a human nucleic-acid associated protein
 CC designated NAAp-16. NAAp sequences have antiparkinsonian, nootropic,
 CC neuroprotective, muscular, neuroleptic, antiinflammatory, immunosuppressive,
 CC cytostatic, dermatological, virucide, antibacterial, fungicide,
 CC anti-allergic, nephrotoxic, antiparasitic, protozoacide, antihelminthic, antiarteriosclerotic,
 CC cardiovascular, gastrointestinal and hepatotoxic activities, and can be
 CC used in gene therapy. The NAAp polypeptide or its fragments, and the
 CC polynucleotide encoding the polypeptide are useful in diagnosing,
 CC preventing, and treating disorders associated with an abnormal expression
 CC or activity of NAAp (nucleic acid-associated protein), such as
 CC neurodegenerative disorders (e.g. Parkinson's disease, Alzheimer's
 CC disease), muscular disorders (e.g. myotonic dystrophy, catatonia),
 CC endocrine disorders (e.g. diabetes, Grave's disease), cancers (e.g.
 CC leukaemia, cervical or breast cancers), immunological disorders (e.g.
 CC scleroderma, systemic lupus erythematosus, allergies), gastrointestinal
 CC disorders (e.g. Crohn's disease), renal disorders (e.g. Goodpasture's
 CC syndrome), infections (e.g. viral, bacterial, fungal, parasitic,
 CC protozoal, helminthic), cardiovascular disorders (e.g. atherosclerosis),
 CC or hepatic diseases (e.g. cirrhosis). NAAp or its fragments may also be
 CC used in screening for compounds that specifically bind to and modulate
 CC the activity of NAAp. The polynucleotides can be used to create humanised
 CC animals or transgenic animals to model human disease.
 XX
 Sequence 948 AA:
 Query Match 62.9%; Score 39; DB 8; length 948;
 Best Local Similarity 72.7%; Pred. No. 2.8e+02;
 Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 Qy 2 IEALPRTHESQ 12
 Db 105 VEALLRHESQ 115
 RESULT 12
 ID ABB1798
 ID ABB1798 standard; peptide; 509 AA.

XX
 AC ABB1179;
 XX 11-JAN-2002 (first entry)
 DT DE Human CGI-41 protein homologue, SEQ ID NO:2168.
 XX Human; cytokine; cell proliferation; cell differentiation; growth factor;
 KW haemopoiesis regulation; tissue growth; immunomodulator; activin;
 KW inhibin; chemotaxis; chemokinesis; thrombolytic; oncogenesis;
 KW proliferation; metatasis; cancer; tumor; haematopoietic disorder;
 KW myeloid cell disorder; lymphoid cell disorder; asthma; arthritis;
 KW chronic inflammatory condition; proliferative retinopathy;
 KW atherosclerosis; coronary heart disease; arterial ischaemia;
 KW bone disorder; osteoporosis; vascular growth disorder;
 KW tissue regeneration; wound healing; infection; immune disorder;
 KW cell culture; drug screening; gene therapy; antiinflammatory;
 KW antiasthmatic; antiarthritic; haemostatic; antiplatelet;
 KW cytostatic; osteopathic; vasotropic; cardiant; virucide; antibacterial;
 KW antifungal; vulnerary; antiulcer.
 XX OS Homo sapiens.
 XX PN WO200157788-A2.
 XX PD 09-AUG-2001.
 XX PR 05-FEB-2001; 2001WO-US003800.
 XX PR 03-FEB-2000; 2000US-00436914.
 XX PR 27-APR-2000; 2000US-00560875.
 XX PA (HYSB-) HYSEQ INC.
 PI Tang YT, Liu C, Drmanac RT;
 PI XX WPI; 2001-457740/49.
 DR N-PSDB; ABB09042.
 XX PT Human proteins and DNA encoding sequences useful for preventing, treating
 PT or ameliorating a medical condition in a mammalian subject e.g. arthritis
 PT and cancer.
 XX PS Claim 20; Page 252; 1963pp; English.

XX Sequences ABB10981-ABB12330 represent 1350 novel human polypeptides, and
 CC sequences ABA08225-ABA09574 represent nucleic acids encoding them. The
 invention also relates to vectors and recombinant host cells comprising a
 CC nucleotide of the invention, methods of producing the novel polypeptides,
 CC antibodies against the polypeptides, methods of detecting the nucleotides
 CC or polypeptides in a sample, and methods of identifying compounds which
 CC bind to polypeptides of the invention. Although novel, many of the
 CC polypeptides of the invention have homology to known proteins, thereby
 giving an insight into their probable biological activities, and hence
 potential therapeutic applications. The polypeptides of the invention may
 have various activities, including cytokine, cell proliferation or cell
 differentiation activities; stem cell growth factor activity;
 CC haemopoiesis regulatory activity; tissue growth activity;
 CC immunomodulatory activity; activin- or inhibin-related activities;
 CC chemotactic or chemoattractant activities; haemostatic, thrombotic or
 CC thrombolytic activities; receptor or ligand activities; or may be
 involved in oncogenesis, cancer cell proliferation or metastasis.
 Depending on their biological activities, polypeptides and nucleotides of
 the invention are useful for preventing, treating or ameliorating medical
 conditions, e.g., by protein or gene therapy. Such conditions include
 CC cancers, haematopoietic disorders (e.g., myeloid or lymphoid cell
 disorders), chronic inflammatory diseases (e.g., asthma or arthritis),
 CC proliferative retinopathy, atherosclerosis, coronary heart disease,
 CC arterial ischaemia, bone disorders (e.g., osteoporosis), and abnormal
 CC vascular growth. Polypeptides involved with tissue regeneration and
 CC repair (or nucleic acids encoding them) may be used to promote wound
 healing (e.g., of burns, incisions and ulcers), while those with
 CC immunomodulatory activities may be used in the treatment of viral,
 XX
 RESULT 13
 ADP64400
 ID ADP64400 standard; protein; 509 AA.
 XX
 ADP64400;
 XX
 DT 12-AUG-2004 (first entry)
 XX DE Trichoderma reesei beta-glucosidase BGL7 precursor protein.
 XX Beta-glucosidase; BGL7; yeast dough; baked food; detergent; aroma; wine;
 KW cellulase; biomass; bio-ethanol; enzyme; EC 3.2.1.21.
 XX OS Hypocrea jecorina.
 XX PH Key
 FT Peptide
 FT Misc-difference⁸
 FT /note= "Encoded by AGG codon of the sequence {seqid:4}"
 FT Protein
 FT /label= Mature_BGL7
 FT Misc-difference⁵²
 FT /note= "Encoded by GGC codon of the sequence {seqid:1}"
 FT Misc-difference⁸⁶
 FT /note= "Encoded by CT codon of the sequence {seqid:1}"
 FT Misc-difference⁹¹
 FT /note= "Encoded by GCC codon of the sequence {seqid:1}"
 FT Misc-difference¹⁷⁷
 FT /note= "Encoded by MC codon of the sequence {seqid:1}"
 FT Misc-difference¹⁷⁷
 FT /note= "Encoded by AGG codon of the sequence {seqid:4}"
 FT Misc-difference²⁰⁷
 FT /note= "Encoded by CGC codon of the sequence {seqid:1}"
 FT Misc-difference²¹⁸
 FT /note= "Encoded by ARG codon of the sequence {seqid:4}"
 FT Misc-difference²⁶⁵
 FT /note= "Encoded by TC codon of the sequence {seqid:1}"
 FT Misc-difference²⁷⁴
 FT /note= "Encoded by CGC codon of the sequence {seqid:1}"
 FT Misc-difference²⁹⁰
 FT /note= "Encoded by TC codon of the sequence {seqid:4}"
 FT Misc-difference⁴⁰¹
 FT /note= "Encoded by GGC codon of the sequence {seqid:4}"
 FT Misc-difference⁴⁰⁷
 FT /note= "Encoded by TAG codon of the sequence {seqid:1}"
 FT Misc-difference⁴²⁶
 FT /note= "Encoded by GGC codon of the sequence {seqid:1}"
 FT Misc-difference⁴⁶²
 FT /note= "Encoded by CGG codon of the sequence {seqid:1}"
 FT Misc-difference⁵¹⁶
 FT /note= "Encoded by UTR codon of the sequence {seqid:4}"
 FT Misc-difference⁵⁸²
 XX
 Query Match 61.3%; Score 38; DB 4; Length 509;
 CC Best Local Similarity 50.0%; Pred. No. 2.2e+02;
 CC Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
 CC
 SQ Sequence 509 AA;
 OQ 1 GIEALPRTH 10
 Db 390 GVQGIPRVHE 399
 CC bacterial and fungal infections in addition to immune disorders.
 CC Polypeptides with growth factor activity may be used in cell cultures to
 CC promote cell growth. For example, such polypeptides may be used to
 CC manipulate stem cell in culture to give rise to neuroepithelial cells
 CC that can be used to augment or replace cells damaged by illness.
 CC autoimmune disease or accidental damage. The polypeptides and nucleotides
 CC may also be used in the diagnosis of the above conditions, and in drug
 CC screening techniques. The present sequence represents a novel human
 CC polypeptide of the invention.

PT Misc-difference 620 /note= "Encoded by AA codon of the sequence {seqid:1}"
 PT Misc-difference 705 /note= "Encoded by GGC codon of the sequence {seqid:4}"
 PT Misc-difference 708 /note= "Encoded by AAG codon of the sequence {seqid:1}"
 PT Misc-difference 741 /note= "Encoded by TT codon of the sequence {seqid:1}"
 PT Misc-difference 755 /note= "Encoded by GGC codon of the sequence {seqid:4}"
 XX US2004102619-A1.
 XX PD 27-MAY-2004.
 XX PR 21-NOV-2002; 2002US-00301015.
 XX PR 21-NOV-2002; 2002US-00301015.
 XX PR (DUNN/) DUNN-COLEMAN N.
 XX PA (WARD/) WARD M.
 XX PI Dunn-Coleman N, Ward M;
 XX DR WPI; 2004-399738/37.
 XX DR N-PSDB; ADP64396, ADP64399, ADP64401.
 XX PT Novel BGL7 polypeptide having beta glucosidase activity useful for improving yeast dough or baked good made from such dough, for preparing detergent compositions or for enhancing potential aroma finished wine product.
 XX PS Claim 18; Fig 2; 25pp; English.
 CC The invention relates to beta-glucosidase BGL7 (EC 3.2.1.21) polypeptide and poly nucleotide from Trichoderma. The enzyme is useful for improving the characteristics of a yeast dough or baked good made from such dough, for preparing detergent composition, for enhancing the potential aroma of finished wine product, for hydrolysis of cellulose to its sugar components, for preparing cellulase composition for use in detergents or for degradation of biomass into sugar for bio-ethanol production. The present sequence is Trichoderma reesei beta-glucosidase BGL7 precursor protein.
 CC Sequence 765 AA;
 CC Query Match 61.3%; Score 38; DB 8; Length 765;
 CC Best Local Similarity 50.0%; Pred. No. 3.4e+02;
 CC Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
 CC Qy 1 GIEALPRTHSQ 12
 CC Db 28 GVSQIPSTHSQ 39
 SQ Sequence 201 AA;
 SQ RESULT 15
 SQ AB071665
 ID AB071665 standard; protein; 241 AA.
 AC AB071665;
 XX DT 29-JUL-2004 (first entry)
 XX DE Pseudomonas aeruginosa polypeptide #3840.
 KW Bacterial infection; Pseudomonas aeruginosa infection; antibacterial.
 KW Pseudomonas aeruginosa.
 OS Pseudomonas aeruginosa.
 OS US6551793-B1.
 XX DT 29-JUL-2004 (first entry)
 XX DE Pseudomonas aeruginosa polypeptide #2689.
 KW Bacterial infection; Pseudomonas aeruginosa infection; antibacterial.
 KW Pseudomonas aeruginosa.
 OS Pseudomonas aeruginosa.
 OS US6551793-B1.
 XX PN 18-FEB-1998; 99US-0074788P.
 XX PR 27-JUL-1998; 98US-0094190P.
 XX PA (GENO-) GENOME THERAPEUTICS CORP.
 XX PI Rubenfield MJ, Nolling J, Deloughery C, Bush D;
 XX DR N-PSDB; AB0d04085.
 XX PT Novel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide, useful as molecular targets for diagnostics, prophylaxis and treatment of pathological conditions resulting from bacterial infection.
 XX PS Disclosure: SEQ ID NO 19260; 455pp; English.
 CC The invention relates to Pseudomonas aeruginosa polypeptides and the polynucleotides encoding them. The sequences are useful in diagnosis and therapy of pathological conditions, as molecular targets for diagnostics, prophylaxis and treatment of pathological condition resulting from a bacterial infection, for evaluating a compound, such as a polypeptide, for the ability to bind a P. aeruginosa nucleic acid, as components of effective antibacterial targets, as targets for antibacterial drugs, including anti-P. aeruginosa drugs, as templates for recombinant production of P. aeruginosa-derived peptides or polypeptides, as target components for diagnosis and/or treatment of P. aeruginosa caused infection, and in detection of P. aeruginosa. Sequences or other sequences of Pseudomonas species using biotech technology. Sequences AB067126-AB084396 represent P. aeruginosa polypeptides of the invention. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format from USPTO at seqdata.uspto.gov/sequence.html
 CC Sequence 201 AA;
 CC Query Match 59.7%; Score 37; DB 7; Length 201;
 CC Best Local Similarity 66.7%; Pred. No. 1.3e+02;
 CC Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 CC Qy 1 GIEALPRTH 9
 CC Db 172 GLRTLPRTH 180
 SQ Sequence 201 AA;
 SQ RESULT 15
 SQ AB071665
 ID AB071665 standard; protein; 241 AA.
 AC AB071665;
 XX DT 29-JUL-2004 (first entry)
 XX DE Pseudomonas aeruginosa polypeptide #3840.
 KW Bacterial infection; Pseudomonas aeruginosa infection; antibacterial.
 KW Pseudomonas aeruginosa.
 OS Pseudomonas aeruginosa.
 OS US6551795-B1.
 XX PN 18-FEB-1998; 99US-00252991.
 XX PR 27-JUL-1998; 98US-0094190P.
 XX PA (GENO-) GENOME THERAPEUTICS CORP.
 XX PI Rubenfield MJ, Nolling J, Deloughery C, Bush D;
 XX DR N-PSDB; AB0d04085.
 XX PT Novel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide, useful as molecular targets for diagnostics, prophylaxis and treatment of pathological conditions resulting from bacterial infection.
 XX PS Disclosure: SEQ ID NO 19260; 455pp; English.
 CC The invention relates to Pseudomonas aeruginosa polypeptides and the polynucleotides encoding them. The sequences are useful in diagnosis and therapy of pathological conditions, as molecular targets for diagnostics, prophylaxis and treatment of pathological condition resulting from a bacterial infection, for evaluating a compound, such as a polypeptide, for the ability to bind a P. aeruginosa nucleic acid, as components of effective antibacterial targets, as targets for antibacterial drugs, including anti-P. aeruginosa drugs, as templates for recombinant production of P. aeruginosa-derived peptides or polypeptides, as target components for diagnosis and/or treatment of P. aeruginosa caused infection, and in detection of P. aeruginosa. Sequences or other sequences of Pseudomonas species using biotech technology. Sequences AB067126-AB084396 represent P. aeruginosa polypeptides of the invention. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format from USPTO at seqdata.uspto.gov/sequence.html
 CC Sequence 201 AA;
 CC Query Match 59.7%; Score 37; DB 7; Length 201;
 CC Best Local Similarity 66.7%; Pred. No. 1.3e+02;
 CC Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 CC Qy 1 GIEALPRTH 9
 CC Db 172 GLRTLPRTH 180
 SQ Sequence 201 AA;
 SQ RESULT 15
 SQ AB071665
 ID AB071665 standard; protein; 241 AA.
 AC AB071665;
 XX DT 29-JUL-2004 (first entry)
 XX DE Pseudomonas aeruginosa polypeptide #3840.
 KW Bacterial infection; Pseudomonas aeruginosa infection; antibacterial.
 KW Pseudomonas aeruginosa.
 OS Pseudomonas aeruginosa.
 OS US6551795-B1.
 XX PN 18-FEB-1998; 99US-00252991.
 XX PR 27-JUL-1998; 98US-0094190P.
 XX PA (GENO-) GENOME THERAPEUTICS CORP.
 XX PI Rubenfield MJ, Nolling J, Deloughery C, Bush D;

PS Disclosure; SEQ ID NO 1494; 21pp + Sequence Listing; English.
XX
CC The invention relates to an isolated nucleic acid detection reagent
CC capable of detecting 1000 or more genes from *Drosophila*. The invention is
CC useful in developmental biology and in elucidating cell signalling and
CC cell-cell interactions in higher eukaryotes for the development of
CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences (ABL1676-ABL3051), expressed DNA
CC sequences (ABL1840-ABL175) and the encoded protein (ABBS7737-
CC ABBS7737). The sequence data for this patent did not form part of the
CC ABBS7737. The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp://ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 307 AA;

PT lateral sclerosis.
 XX
 PS Claim 20; SEQ ID NO 488; 300pp; English.
 XX
 CC The present invention relates to the isolation of novel human poly nucleotide sequences and their encoding polypeptides. The novel polypeptides exhibit activities relating to angiogenesis, cytokine, cell proliferation, cell differentiation, antiinflammatory, and stem cell growth factor activities. The polypeptides are involved in the proliferation, differentiation and survival of pluripotent and totipotent stem cells, and are useful for re-engineering damaged or diseased tissues, transplantation, manufacture of bio-pharmaceuticals and development of bio-sensors. The polypeptides can be used to manipulate stem cells in culture to give rise to neuroepithelial cells that can be used to augment or replace cells damaged by illness, autoimmune disease, accidental damage or genetic disorders. The polypeptides induce the proliferation of neural cells and regeneration of nerve and brain tissue and are useful for the treatment of central and peripheral nervous system diseases and neuropathies, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis (ALS). The polypeptides are also involved in chemotactic or chemokinetic activity, regulation of haemopoiesis and are useful for treating myeloid or lymphoid cell disorders, platelet disorders such as thrombocytopaenia and for regeneration of bone, cartilage, tendon, ligament and/or nerve tissue growth, in tissue repair, healing of burns, incisions, ulcers, for treating osteoporosis, osteoarthritis, bone degenerative disorders, and periodontal disease. The polypeptides are also useful for gut protection or regeneration and treatment of lung or liver fibrosis, reperfusion injury in various tissues, various immune deficiencies and disorders including severe combined immunodeficiency (SCID), bacterial or fungal infections, autoimmune disorders (e.g. multiple sclerosis, rheumatoid arthritis, diabetes mellitus, myasthenia gravis), allergic reactions and conditions, such as asthma or other respiratory problems. The polypeptides are involved in thrombolytic or thrombosis and are useful in treatment of various coagulation disorders (including hereditary disorders such as haemophilia) or to enhance coagulation and other haemostatic events in treating wounds resulting from trauma, surgery or other causes. The polypeptides exhibit immune stimulating or immune suppressing activity, and are useful for treating autoimmune diseases or cancer. They also inhibit the growth, infection or function of infectious cycles of rhythms, fertility of male or female subjects, metabolism, catabolism, and anabolism. ABO00414-ABO00749 represent the novel polypeptides of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp://wipo.int/pub/published_pct_sequences

XX SQ Sequence 410 AA;

Query Match 59.7%; Score 37; DB 6; Length 410;
 Best Local Similarity 60.0%; Pred. No. 2.7e+02;
 Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
 OQ QY 1 GIEALPRTRESQ 12
 Db 422 GIEVVRLLHQSQ 433

RESULT 19
 ABP41544
 ID ABP41544 Standard; protein; 126 AA.
 XX
 AC ABP41544;
 XX
 DT 22-AUG-2002 (first entry)
 XX DB Human ovarian antigen HCOPQ33, SEQ ID NO:2676.
 XX Human; ovarian antigen; ovary; ovarian; breast; cancer; tumour;
 KW ovarian cancer; breast cancer; tumour; reproductive system disorder;
 KW infertility; pregnancy disorder; anovulation; polycystic ovary syndrome;
 KW PCOS; ovarian; cyst; dysmenorrhoea; endocrine disorder; infection;
 KW inflammatory condition; immune disorder; blood disorder;
 KW cardiovascular disorder; respiratory disorder; neurological disorder;
 KW gastrointestinal disorder; urinary system disorder; drug screening;
 KW gene therapy; chromosome mapping; forensic analysis;
 KW antibody preparation; cytostatic; immunomodulatory; neuroprotective;
 KW antiinflammatory; gynaecological; reproductive.
 XX OS Homo sapiens.
 XX
 AC WO200200677-A1.
 XX
 DT 03-JAN-2002.
 XX
 ID 07-JUN-2001; 2001WO-US010569.
 XX
 PR 07-JUN-2000; 2000US-0203467P.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.

XX OS Klebsiella pneumoniae.

RESULT 18
 ABO64452
 ID ABO64452 standard; protein; 568 AA.
 XX
 AC ABO64452;
 XX
 DT 29-JUL-2004 (first entry)

XX DE Klebsiella pneumoniae polypeptide seqid 10969.
 XX
 KW Recombinant expression vector; transcription regulatory element;
 KW Klebsiella pneumoniae protein; antibacterial; Vaccine.
 XX
 OS Klebsiella pneumoniae.

XX US6610836-B1.
 PN XX
 PD 26-AUG-2003.
 XX PR 27-JAN-2000; 2000US-00489039.
 XX PR 29-JAN-1999; 99US-0117747P.
 XX PA (GENO-) GENOME THERAPEUTICS CORP.
 XX PR Bretton GL, Osborne M;
 XX DR WPI; 2003-895346/82.
 XX N-PSDB; ACH98003.
 XX PT preparing a vaccine composition against Klebsiella pneumoniae.
 XX Disclosure; SEQ ID NO 10969; 932pp; English.
 CC The invention describes a new isolated nucleic acid encoding a Klebsiella pneumoniae polypeptide. Also described are: a recombinant expression vector comprising the nucleic acid, operably linked to a transcription regulatory element; and a cell comprising the recombinant expression vector. The nucleic acid is useful for preparing a vaccine composition against Klebsiella pneumoniae. This is the amino acid sequence of a Klebsiella pneumoniae polypeptide of the invention

XX SQ Sequence 568 AA;

Query Match 59.7%; Score 37; DB 7; Length 568;
 Best Local Similarity 58.3%; Pred. No. 3.8e+02;
 Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

XX	Bisse CE, Rozen CA;	07-FEB-2002; 2002WO-IB003040.
DR	WPI: 2002-147078/19.	XX
XX	N-ISDB; ABQ5421.	PR 07-FEB-2001; 2001FR-00001659.
PT	Isolated nucleic acid molecules encoding novel ovarian polypeptides, useful in the prevention, treatment and diagnosis of cancer (e.g. ovarian cancer), immune disorders, cardiovascular disorders and neurological diseases.	XX
PT	Claim 11, SEQ ID NO 2676; 2922pp; English.	PA (INSP) INST PASTEUR.
XX	The invention relates to 2175 novel human ovarian antigens (ABP41054-ABP43228) and to cDNA encoding them (ABP5411-ABP56305), and also encompasses polypeptides 90% identical to the sequences of the invention. The invention additionally relates to recombinant vectors and host cells comprising human ovarian antigen polymonucleotides, antibodies against human ovarian antigens, and the use of ovarian antigen polymonucleotides and polypeptides in diagnosing, treating, prognosis or preventing various ovary and/or breast-related disorders. Such conditions include ovarian cancer and breast cancer, and metastatic tumours of ovarian or breast origin, reproductive system disorders (e.g., infertility, disorders of pregnancy, anovulation, polycystic ovary syndrome, ovarian cysts, and dysmenorrhoea), endocrine disorders, infections (e.g., chlamydia, HIV, toxoplasmosis, and toxic shock syndrome), inflammatory conditions (e.g., mastitis, oophoritis and vaginitis), immune disorders (e.g., congenital and acquired immunodeficiencies, autoimmune oophoritis, systemic lupus erythematosus), blood-related disorders (e.g., anaemia), cardiovascular disorders, respiratory disorders, neurological disorders, gastrointestinal disorders and urinary system disorders. Ovarian antigen polypeptides and polynucleotides may also be used in screening for compounds which modulate ovarian antigen expression or activity. The polynucleotides may further be used for gene therapy, chromosome mapping, in the identification of individuals and in forensic analysis, and the polypeptides may be used as food additives or to prepare antibodies useful in disease diagnosis, drug targeting and phenotyping. The present sequence represents a human ovarian antigen of the invention. Note: the specification, but was obtained in electronic format directly from WIPO at http://wipo.int/pub/published_pct_sequences	PA (CNRS) CNRS CENT NAT. RECH SCI.
PS	SQ Sequence 126 AA:	XX PI Duchaud E, Taourit S, Glaser P, Frangeul L, Kunst F, Danchin A;
XX	Query Match 58.1%; Score 36; DB 5; Length 126; Best Local Similarity 41.7%; Pred. No. 1.2e+02; Mismatches 5; Conservative 4; Indels 0; Gaps 0;	XX PI Buchrieser C;
QY	1 GIEALPRTHESQ 12	XX DR WPI: 2003-148459/14.
Db	102 GVPSTIPQTHSPQ 113	XX PT Genomic sequence of <i>Photobacterium luminescens</i> and encoded polypeptides, useful e.g. as therapeutic antimicrobials and agricultural pesticides.
RESULT 20	ABM69852 standard; protein; 152 AA.	XX PS Claim 2; SEQ ID NO 2949; 1205pp; French.
ID	ABM69852;	XX The invention relates to the isolation of genes and their encoded proteins from <i>Photobacterium luminescens</i> . The isolated genes are sources of probes and primers for detecting the genome of <i>P. luminescens</i> and related species, to study polymorphisms; for gene analysis and for detection/amplification of the genes. Antibodies (Ab) raised against the polypeptides encoded by the genes are used for detection/identification of <i>P. luminescens</i> , e.g. in foods. The genes, proteins, Ab and cells that carry a gene-containing vector are used to select compounds that modulate, regulate, induce or inhibit expression of the genes in plants, animals or microorganisms other than <i>P. luminescens</i> and are able to alter response or sensitivity to toxins and antibiotics produced by <i>P. luminescens</i> . Cells transformed to express the genes are useful for recombinant production of the proteins, particularly toxins and antibacterials useful as insecticides, bactericides and fungicides. The proteins, vectors containing the genes and Ab are also useful therapeutically (to treat microbial infection by bacteria or fungi that are sensitive to <i>P. luminescens</i> -encoded toxins or antibiotics) and as biopesticides. Other uses of the genes and the proteins are as virulence factors and for identifying targets of human diseases for which <i>P. luminescens</i> is a model (particularly plague and whooping cough). This sequence represents one of the isolated <i>P. luminescens</i> proteins
XX	Sequence 152 AA:	XX SQ Sequence 152 AA:
Query Match 58.1%; Score 36; DB 6; Length 152; Best Local Similarity 77.8%; Pred. No. 1.5e+02; Mismatches 7; Conservative 1; Indels 0; Gaps 0;	Query Match 58.1%; Score 36; DB 6; Length 152; Best Local Similarity 77.8%; Pred. No. 1.5e+02; Mismatches 7; Conservative 1; Indels 0; Gaps 0;	XX
XX	ABM69852 standard; protein; 152 AA.	XX
AC	ABM69852;	XX
DT	20-NOV-2003 (first entry)	XX
XX	Photorhabdus luminescens protein sequence #2949.	XX
DE	Antibacterial; fungicide; insecticide; polymorphism; genetic analysis; detection; food; gene expression; plant; animal; microorganism; toxin; antibiotic; biopesticide; virulence factor; disease model; plague; whooping cough.	XX
XX	Photorhabdus luminescens.	XX
OS	Photorhabdus luminescens.	XX
PN	WO200294867-A2.	XX
XX	28-NOV-2002.	XX
PD	07-FEB-2002; 2002WO-IB003040.	XX
PP	28-NOV-2002.	XX

XX
 PR 07-FEB-2001; 2001FR-00001659.
 XX
 PA (INSP) INST PASTEUR.
 PA (CNRS) CNRS CENT NAT RECH SCI.
 XX
 PI Duchaud E, Taourit S, Glaser P, Frangeul L, Kunst F, Danchin A;
 PI Buchrieser C;
 XX DR WPI; 2003-148459/14.
 XX
 PT Genomic sequence of *Photobacterium luminescens* and encoded polypeptides, useful e.g. as therapeutic antimicrobials and agricultural pesticides.
 XX
 PS Claim 2; SEQ ID NO 2878; 1205pp; French.
 XX
 CC The invention relates to the isolation of genes and their encoded proteins from *Photobacterium luminescens*. The isolated sequences are sources of probes and primers for detecting the genome of *P. luminescens* and related species; to study polymorphisms; for gene analysis and for detection/amplification of the genes. Antibodies (Ab) raised against the polypeptides encoded by the genes are used for detection/identification of *P. luminescens*, e.g. in foods. The genes/proteins Ab and cells that carry a gene-containing vector are used to select compounds that modulate, regulate, induce or inhibit expression of the genes in plants, animals or microorganisms other than *P. luminescens* and are able to alter response or sensitivity to toxins and antibiotics produced by *P. luminescens*. Cells transformed to express the genes are useful for recombinant production of the proteins, particularly toxins and antibacterials useful as insecticides, bactericides and fungicides. The genes, proteins, vectors containing the genes and Ab are also useful therapeutically (to treat microbial infection by bacteria or fungi that are sensitive to *P. luminescens*-encoded toxins or antibiotics) and as biopesticides. Other uses of the genes and the proteins are as virulence factors and for identifying targets of human diseases for which *P. luminescens* is a model (particularly plague and whooping cough). This sequence represents one of the isolated *P. luminescens* proteins.
 XX
 SQ Sequence 152 AA;

Query Match	58.1%	Score	36;	DB	6;	Length	152;
Best Local Similarity	77.8%	Pred.	No. 1.	Se-02;	1;	Indels	0;
Matches	7;	Conservative	1;	Mismatches	0;	Gaps	0;

QY 3 BALPRTHES 11
 Db 96 EALKTHEA 104

RESULT 22
 ADK16367 ID ADK16367 standard; protein; 179 AA.
 XX
 AC ADK16367;
 AC ADK16367;
 AC ADK16367;
 DT 06-MAY-2004 (first entry)
 DE Nanoarchaeum equitans cancer-associated (CA) protein #159.
 KW cancer-associated gene; CA gene; cancer; carcinoma; lymphoma; leukaemia.
 KW Nanoarchaeum equitans.
 OS Homo sapiens.
 XX PN WO200153312-A1.
 XX PD 26-JUL-2001.
 XX PIP 26-BC-2000; 200000-US034263.
 XX PR 23-DEC-1999; 990US-00471275.
 PR 21-JAN-2000; 20000US-00488725.
 PR 25-APR-2000; 2000US-0052317.
 PR 20-JUN-2000; 20000US-00598042.
 PR 19-JUL-2000; 20000US-00620312.
 PR 03-AUG-2000; 2000US-00653450.
 PR 14-SEP-2000; 20000US-00662191.
 PR 19-OCT-2000; 20000US-00693036.
 PR 29-NOV-2000; 2000US-00727344.
 XX
 PA (HYSB-) HYSEQ INC.
 XX
 PI Tang YR, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D, Zhao QA;
 PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J, Zhao QA;
 PI Zhou P, Goodrich R, Drmanac RT;
 XX DR WPI; 2001-442253/47.
 DR N-PSDB; AAI59879.

XX Novel nucleic acids and polypeptides, useful for treating disorders such
 PT as central nervous system injuries.
 XX
 PS Example 2; SEQ ID NO 5654; 10078pp; English.

The invention relates to human nucleic acids (AA15779-AA16136) and the
 CC encoded polypeptides (ADM38642-AM42213) with nootropic,
 CC immunosuppressant and cytotoxic activity. The polynucleotides are useful
 CC in gene therapy. A composition containing a polypeptide or polynucleotide
 CC of the invention may be used to treat diseases of the peripheral nervous
 CC system, such as peripheral nervous injuries, peripheral neuropathy and
 CC localized neuropathies and central nervous system diseases, such as
 CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
 CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
 CC utilisation of the activities such as: immune system suppression,
 CC and thrombolytic activity, chemotactic/chemokinetic activity, haemostatic
 CC assays for receptor activity, arthritis and inflammation, leukemias and
 CC C.N.S disorders. Note: The sequence data for this patent did not form
 CC part of the printed specification

SQ Sequence 198 AA;

Query Match 58.1%; Score 36; DB 4; Length 198;
 Best Local Similarity 58.3%; Pred. No. 1.9e+02; Mismatches 7; Indels 4; Gaps 0; Matches 1;

OY 1 GIEALPRTHESQ 12
 Db 128 GIDFPRPLHRSQ 139

RESULT 24
 AB072967 standard; protein; 251 AA.

OY 1 GIEALPRTHESQ 12
 Db 128 GIDFPRPLHRSQ 139

RESULT 24
 AB072967 standard; protein; 251 AA.

OY 1 GIEALPRTHESQ 12
 Db 128 GIDFPRPLHRSQ 139

RESULT 24
 AB072967 standard; protein; 251 AA.

OY 1 GIEALPRTHESQ 12
 Db 128 GIDFPRPLHRSQ 139

RESULT 24
 AB072967 standard; protein; 251 AA.

OY 1 GIEALPRTHESQ 12
 Db 128 GIDFPRPLHRSQ 139

RESULT 24
 AB072967 standard; protein; 251 AA.

OY 1 GIEALPRTHESQ 12
 Db 128 GIDFPRPLHRSQ 139

RESULT 24
 AB072967 standard; protein; 251 AA.

OY 1 GIEALPRTHESQ 12
 Db 128 GIDFPRPLHRSQ 139

RESULT 24
 AB072967 standard; protein; 251 AA.

OY 1 GIEALPRTHESQ 12
 Db 128 GIDFPRPLHRSQ 139

RESULT 24
 AB072967 standard; protein; 251 AA.

OY 1 GIEALPRTHESQ 12
 Db 128 GIDFPRPLHRSQ 139

RESULT 24
 AB072967 standard; protein; 251 AA.

OY 1 GIEALPRTHESQ 12
 Db 128 GIDFPRPLHRSQ 139

RESULT 24
 AB072967 standard; protein; 251 AA.

OY 1 GIEALPRTHESQ 12
 Db 128 GIDFPRPLHRSQ 139

RESULT 24
 AB072967 standard; protein; 251 AA.

OY 1 GIEALPRTHESQ 12
 Db 128 GIDFPRPLHRSQ 139

RESULT 24
 AB072967 standard; protein; 251 AA.

OY 1 GIEALPRTHESQ 12
 Db 128 GIDFPRPLHRSQ 139

RESULT 24
 AB072967 standard; protein; 251 AA.

OY 1 GIEALPRTHESQ 12
 Db 128 GIDFPRPLHRSQ 139

RESULT 24
 AB072967 standard; protein; 251 AA.

OY 1 GIEALPRTHESQ 12
 Db 128 GIDFPRPLHRSQ 139

CC bacterial infection, for evaluating a compound such as a polypeptide,
 CC for the ability to bind a P. aeruginosa nucleic acid, as components of
 CC effective antibacterial targets, as targets for antibacterial drugs,
 CC including anti-P. aeruginosa drugs, as templates for recombinant
 CC production of P. aeruginosa-derived peptides or polypeptides, as target
 CC components for diagnosis and/or treatment of P. aeruginosa-caused
 CC infection, and in detection of P. aeruginosa sequences or other sequences
 CC of Pseudomonas species using biochip technology. Sequences AB067825-
 CC AB04396 represent P. aeruginosa polypeptides of the invention. Note: The
 CC sequence data for this patent did not form part of the printed
 CC specification but was obtained in electronic format from USPTO at
 CC seqdata.uspto.gov/sequence.html

CC Sequence 251 AA;

Query Match 58.1%; Score 36; DB 7; Length 251;
 Best Local Similarity 66.7%; Pred. No. 2.5e+02; Mismatches 6; Indels 0; Gaps 0; Matches 1;

OY 2 IEALPRTHE 10
 Db 20 VEQAPRTHE 28

RESULT 25
 ABU21788
 ID ABU21788 standard; protein; 336 AA.

XX
 AC ABU21788;
 XX
 DT 19-JUN-2003 (first entry)
 DE Protein encoded by Prokaryotic essential gene #7315.
 KW Antisense; prokaryotic essential gene; cell proliferation; drug design.
 OS Burkholderia fungorum.
 XX
 PN WO200277183-A2.
 XX
 PD 03-OCT-2002.
 XX
 PF 21-MAR-2002; 2002WO-US0909107.
 XX
 PR 21-MAR-2001; 2001US-00815242.
 PR 06-SEP-2001; 2001US-00948939.
 PR 25-OCT-2001; 2001US-034293P.
 PR 08-FEB-2002; 2002US-00072851.
 PR 06-MAR-2002; 2002US-0362699P.
 XX
 PA (ELIT-) ELITRA PHARM INC.

XX Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW,
 PI Wall D, Travick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH,
 XX
 DR MPI; 2003-02926/02.
 DR N-PSDB; ACA25658.

PT New antisense nucleic acids, useful for identifying proteins or screening
 PT for homologous nucleic acids required for cellular proliferation to
 PT isolate candidate molecules for rational drug discovery programs.

XX
 PS Claim 25; SEQ ID NO 49712; 176pp; English.

XX The invention relates to an isolated nucleic acid comprising any one of
 CC the 6213 antisense sequences given in the specification where expression
 CC of the nucleic acid inhibits proliferation of a cell. Also included are:
 CC (1) a vector comprising a promoter operably linked to the nucleic acid
 CC encoding a polypeptide whose expression is inhibited by the antisense
 CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
 CC polypeptide or its fragment whose expression is inhibited by the
 CC antisense nucleic acid; (4) an antibody capable of specifically binding
 CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular

CC proliferation or the activity of a gene in an operon required for
 CC proliferation; (7) identifying a compound that influences the activity of
 CC the gene product or that has an activity against a biological pathway
 CC required for proliferation, or that inhibits cellular proliferation; (8)
 CC identifying a gene required for cellular proliferation or the biological
 CC pathway in which a proliferation-required gene or its gene product lies
 CC or a gene on which the test compound that inhibits proliferation of an
 CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
 CC compound's activity; (11) a culture comprising strains in which the gene
 CC product is overexpressed or underexpressed; (12) determining the extent
 CC to which each of the strains is present in a culture or collection of
 CC strains; or (13) identifying the target of a compound that inhibits the
 CC proliferation of an organism. The antisense nucleic acids are useful for
 CC identifying proteins or screening for homologous nucleic acids required
 CC for cellular proliferation to isolate candidate molecules for rational
 CC drug discovery programs, or for screening homologous nucleic acids
 CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,
 CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of
 CC the target prokaryotic essential genes. Note: The sequence data for this
 CC patent did not form part of the printed specification, but was obtained
 CC in electronic format directly from WIPO at
 CC [fpp.wipo.int/Pub/published_pct_sequences](http://www.wipo.int/Pub/published_pct_sequences)
 SQ Sequence 336 AA:
 Query Match 58.1%; Score 36; DB 6; Length 336;
 Best Local Similarity 50.0%; Pred. No. 3.4e+02;
 Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0
 Ov 1 GIEAMPRTTHE 10
 Qv |:| :|||:
 Db 146 GVEEIPREHQ 155

RESULT 26
 AAB65995 58.1%; Score 36; DB 6; Length 336;
 ID AAB65995 standard; protein; 365 AA.
 XX
 AC AAB65995;
 XX
 DT 03-APR-2001 (first entry)
 DE Human secreted protein BLAST search protein SEQ ID NO: 135.
 XX
 KW Cytostatic; immunosuppressive; notropic; neuroprotective; antiviral;
 KW antiallergic; hepatotropic; antidiabetic; antiinflammatory; antiulcer;
 KW vulnerary; anticonvulsant; antibacterial; antifungal; antiparasitic;
 KW cardiac; gene therapy; cancer; immune disorder; cardiovascular disorder;
 KW neurological disease; infection; human; secreted protein.
 OS Homo sapiens.
 XX
 PN WO20007023-A1.
 XX
 PD 21-DEC-2000.
 PR 01-JUN-2000; 2000WO-US014964.
 XX
 PR 11-JUN-1999; 99US-013B627P.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Rosen CA, Ruben SM, Komatsoulis GA;
 XX
 DR WPI; 2001-032308/04.
 PT Isolated nucleic acid molecule encoding a human secreted protein is used
 PT in preventing, treating or ameliorating a medical condition.
 PS Disclosure; Page 537-538; 558PP; English.
 CC The invention relates to the isolation of genes AAF45072-F45120 encoding
 CC the human secreted proteins AAB65920-B65568. This sequence represents a

CC peptide fragment homologous to the protein encoded by the gene given in the descriptor line. The sequence is a search result from a BLASTX homology search. The genes and proteins are useful for preventing, ameliorating or treating medical conditions, e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant)agonists are useful in the diagnosis, treatment and prevention of:
 (a) cancer, e.g. breast and ovarian cancer, and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders e.g. Addison's disease, allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c) cardiovascular disorders such as myocardial ischaemias; (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f) infectious diseases such as viral, bacterial, fungal and parasitic infections

CC antibodies and (ant)agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer, and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders e.g. Addison's disease, allergies, autoimmune haemolytic anaemia, autoimmune rheumatoid arthritis and ulcerative colitis; (c) cardiovascular disorders such as myocardial ischaemia; (d) wound healing; (e) neurological diseases such as e.g. cerebral anoxia and epilepsy; and (f) infectious diseases such as viral, bacterial, fungal and parasitic infections

SQ Sequence 366 AA;

Query Match 58.1%; Score 36; DB 4; Length 366;
Best Local Similarity 50.0%; Pred. No. 3.7e+02; Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 GIEALPRTRHESQ 12
DB 124 GKOAMPEKHESE 135

RESULT 28

ID ADS22625 standard; protein; 403 AA.
XX AC ADS22625;

DT 02-DEC-2004 (first entry)

DE Bacterial polypeptide #11658.

XX KW Recombinant DNA construct; transformed plant; improved plant property; cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis; pathogen tolerance; pest tolerance; plant disease resistance; cell cycle pathway modification; plant growth regulator; homologous recombination; seed oil yield; protein yield; carbohydrate; KW nitrogen; phosphorus; photosynthesis; lignin; galactomannan; OS bacterial polypeptide.

XX PN US2003233675-A1.

XX PD 18-DEC-2003.

XX PP 20-FEB-2003; 2003US-00369493.

PR 21-FEB-2002; 2002US-0360039P.
XX PA (CAOY/) CAO Y.
PA (HINKL/) HINKLE G J.
PA (ISLAT/) SLATER S C.
PA (CHEN/) CHEN X.
(GOLD/) GOLDMAN B S.

XX PI Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;

XX DR WPI; 2004-061375/06.

XX PT New recombinant DNA construct comprising a promoter positioned to provide expression of a polynucleotide encoding a polypeptide from a microbial source. The invention also relates to a transformed plant comprising the recombinant DNA construct and a method of producing a transformed plant having an improved property. The plant is a crop plant such as maize or soybean. The method of producing a transformed plant

CC having an improved property comprises transforming a plant with the recombinant DNA construct and growing the transformed plant, where the polynucleotide or polypeptide is useful for improving plant properties. CC The recombinant DNA construct is useful for producing plants with improved plant properties, e.g. improved cold, heat or drought tolerance, tolerance to herbicides, extreme osmotic conditions, pathogens or pests, increased resistance to plant disease, better growth rate by modification of the cell cycle pathway with plant growth regulators, increased rate of homologous recombination, modified seed oil or protein yield and/or content, improved yield by modification of carbohydrate, nitrogen or phosphorus use and/or uptake, by modification of photosynthesis or by providing improved plant growth and development under at least one stress condition, improved lignin production or improved galactomannan production. This sequence represents a bacterial polypeptide used in the scope of the invention. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format from USPTO at seqdata.uspto.gov/sequence.html.

SQ Sequence 403 AA;
Query Match 58.1%; Score 36; DB 8; Length 403;
Best Local Similarity 70.0%; Pred. No. 4.1e+02; Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 IEALPRTRHES 11
DB 130 ITGLIPRNHES 139

RESULT 29

ID ADS25515 standard; protein; 403 AA.
XX AC ADS25515;

DT 02-DEC-2004 (first entry)

DE Bacterial polypeptide #14548.
XX KW Recombinant DNA construct; transformed plant; improved plant property; cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis; pathogen tolerance; pest tolerance; plant disease resistance; cell cycle pathway modification; plant growth regulator; carbohydrate; homologous recombination; seed oil yield; protein yield; carbohydrate; nitrogen; phosphorus; photosynthesis; lignin; galactomannan; bacterial polypeptide.

XX OS Bacteria.

XX PN US2003233675-A1.
XX PD 18-DEC-2003.

XX PP 20-FEB-2003; 2003US-00369493.

XX PR 21-FEB-2002; 2002US-0360039P.
XX PA (CAOY/) CAO Y.
PA (HINKL/) HINKLE G J.
PA (ISLAT/) SLATER S C.
PA (CHEN/) CHEN X.
(GOLD/) GOLDMAN B S.

XX PI Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;

XX DR WPI; 2004-061375/06.

XX PT New recombinant DNA construct comprising a promoter positioned to provide expression of a polynucleotide encoding a polypeptide from a microbial source, useful for producing plants with improved properties. XX PS Claim 1; SEQ ID NO 11658; 122pp; English.

CC The invention relates to a recombinant DNA construct comprising a promoter functional in a plant cell, where the promoter is positioned to provide for expression of a polynucleotide encoding a polypeptide from a microbial source. The invention also relates to a transformed plant comprising the recombinant DNA construct and a method of producing a transformed plant having an improved property. The plant is a crop plant such as maize or soybean. The method of producing a transformed plant

The invention relates to a recombinant DNA construct comprising a promoter functional in a plant cell, where the promoter is positioned to provide for expression of a polynucleotide encoding a polypeptide from a microbial source. The invention also relates to a transformed plant comprising the recombinant DNA construct and a method of producing a transformed plant having an improved property. The plant is a crop plant such as maize or soybean. The method of producing a transformed plant having an improved property comprises transforming a plant with the recombinant DNA construct and growing the transformed plant, where the polynucleotide or polypeptide is useful for improving plant properties. The recombinant DNA construct is useful for producing plants with improved plant properties, e.g. improved cold, heat or drought tolerance, tolerance to herbicides, extreme osmotic conditions, pathogens or pests, increased resistance to plant disease, better growth rate by modification of the cell cycle pathway with plant growth regulators, increased rate of homologous recombination, modified seed oil or protein yield and/or content, improved yield by modification of carbohydrate, nitrogen or phosphorus use and/or uptake, by modification of photosynthesis or by providing improved plant growth and development under at least one stress condition, improved lignin production or improved galactomannan production. This sequence represents a bacterial polypeptide used in the scope of the invention. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format from USPTO at seqdata.uspto.gov/sequence.html.

Sequence 403 AA;

Query Match 58.1%; Score 36; DB 8; Length 403;
Best Local Similarity 70.0%; Pred. No. 4.1e+02; Mismatches 0; Indels 0; Gaps 0;

Qy 2 IEALPRTHES 11
Db 130 ITGLPRRNHES 139

RESULT 30

ID ADS26083 Standard; protein; 403 AA.
AC ADS26083;
XX

DT 02-DEC-2004 (first entry)
XX
DE Bacterial polypeptide #15116.
XX
KW Recombinant DNA construct; transformed plant; improved plant property; cold tolerance; heat tolerance; drought tolerance; herbicide; oomosis; pathogen tolerance; pest tolerance; plant disease resistance; cell cycle pathway modification; plant growth regulator; homologous recombination; seed oil yield; protein yield; carbohydrate; nitrogen; phosphorus; photosynthesis; lignin; galactomannan; bacterial polypeptide.
XX
'Bacteria.
XX
OS
PN US2003233675-A1.
XX
PD 18-DEC-2003.
PP 20-FEB-2003; 2003US-00369493.
PR 21-FEB-2002; 2002US-0360039P.
XX
PA (CAOV/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
XX
PI Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;
XX
DR WPI; 2004-061375/06.

New recombinant DNA construct comprising a promoter positioned to provide for expression of a polynucleotide encoding a polypeptide from a microbial source, useful for producing plants with improved properties.

XX
PT
PT
microbial source, useful for producing plants with improved properties.

XX
PS
Claim 1; SEQ ID NO 15116; 122pp; English.

The invention relates to a recombinant DNA construct comprising a promoter functional in a plant cell, where the promoter is positioned to provide for expression of a polynucleotide encoding a polypeptide from a microbial source. The invention also relates to a transformed plant comprising the recombinant DNA construct and a method of producing a transformed plant having an improved property. The plant is a crop plant such as maize or soybean. The method of producing a transformed plant having an improved property comprises transforming a plant with the recombinant DNA construct and growing the transformed plant, where the polynucleotide or polypeptide is useful for improving plant properties. The recombinant DNA construct is useful for producing plants with improved plant properties, e.g. improved cold, heat or drought tolerance, tolerance to herbicides, extreme osmotic conditions, pathogens or pests, increased resistance to plant disease, better growth rate by modification of the cell cycle pathway with plant growth regulators, increased rate of homologous recombination, modified seed oil or protein yield and/or content, improved yield by modification of carbohydrate, nitrogen or phosphorus use and/or uptake, by modification of photosynthesis or by providing improved plant growth and development under at least one stress condition, improved lignin production or improved galactomannan production. This sequence represents a bacterial polypeptide used in the scope of the invention. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format from USPTO at seqdata.uspto.gov/sequence.html.

Sequence 403 AA;

Query Match 58.1%; Score 36; DB 8; Length 403;
Best Local Similarity 70.0%; Pred. No. 4.1e+02; Mismatches 0; Indels 0; Gaps 0;

Qy 2 IEALPRTHES 11
Db 130 ITGLPRRNHES 139

Search completed: August 1, 2005, 08:45:20
Job time : 172 secs

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GenCore version 5.1.6
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On protein - protein search, using BW model

Run on: August 1, 2005, 08:48:30 : Search time 155 Seconds

(without alignments)
 30.163 Million cell updates/sec

Title: US-10-663-749-18

Perfect score: 62

Sequence: 1 GIBALPRTHESQ 12

Scoring table: BL0SUM62

Gapop 10.0 , Gapext: 0.5

Searched: 1745140 seqs, 389608008 residues

Total number of hits satisfying chosen parameters:

1745140

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
 Listing first 150 summaries

Database :

Published Applications_AA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	62	100.0	12 15 US-10-663-749-18	Sequence 18, Appl
2	62	100.0	14 15 US-10-663-749-20	Sequence 20, Appl
3	62	100.0	237 15 US-10-663-749-11	Sequence 11, Appl
4	62	100.0	237 15 US-10-663-749-11	Sequence 11, Appl
5	62	100.0	15 US-10-2363-031B-34	Sequence 34, Appl
6	62	100.0	15 US-10-608-536-15	Sequence 15, Appl
7	62	100.0	15 US-10-663-749-15	Sequence 15, Appl
8	62	100.0	17 US-10-923-348-2	Sequence 2, Appl
9	61	66.1	12 15 US-10-663-749-19	Sequence 19, Appl
10	64.5	36.0	15 US-10-425-115-68790	Sequence 27430, Appl
11	64.5	36.0	US-10-739-930-6590	Sequence 6590, Ap

12	38	61.3	61	15 US-10-424-599-269929	Sequence 269929,
13	38	61.3	117	16 US-10-425-115-22269	Sequence 22269,
14	38	61.3	161	16 US-10-425-115-342771	Sequence 342771,
15	38	61.3	179	16 US-10-425-115-286760	Sequence 386760,
16	38	61.3	509	15 US-10-301-015-2	Sequence 2168, Ap
17	38	61.3	765	16 US-10-425-115-269133	Sequence 26133,
18	37	59.7	69	16 US-10-425-115-303772	Sequence 573, Ap
19	37	59.7	410	15 US-10-243-552-573	Sequence 4912, Ap
20	36	58.1	101	16 US-10-427-963-110387	Sequence 110387,
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22	36	58.1	126	15 US-10-265-049-2675	Sequence 2766, Ap
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26	36	58.1	398	16 US-10-427-930-7940	Sequence 7940, Ap
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71	35	56.5	691	16 US-10-427-930-7223	Sequence 7223, Ap
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73	35	56.5	812	16 US-10-423-963-192780	Sequence 192780,
74	35	56.5	1274	9 US-09-746-491-12	Sequence 12,
75	35	56.5	1615	15 US-10-343-710-10	Sequence 108, Ap
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82	34	54.8	100	11 US-09-864-408A-3234	Sequence 3234, Ap
83	34	54.8	128	16 US-10-427-701-40805	Sequence 40805, A
84	34	54.8	16	US-10-767-701-32836	Sequence 32836, A

ALIGNMENTS

RESULT 1
US-10-663-749-18

US-10-608-536-11
Sequence 11, Application US/10608536
Publication No. US20040049015A1
GENERAL INFORMATION:
APPLICANT: TANABE, Tadashi
TITLE OF INVENTION: PROSTACYCLIN SYNTHASE DERIVED FROM HUMAN
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: SUGIRUE, MION, ZINN, MACPEAK & SEAS
STREET: 2100 Pennsylvania Avenue, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20037

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/608, 536
FILING DATE: 30-Jun-2003
CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/578, 709
FILING DATE: 28-DEC-1995
APPLICATION NUMBER: PCT/JP95/00838
FILING DATE: 27-APR-1995
APPLICATION NUMBER: JP 114316/1994
FILING DATE: 28-APR-1994

ATTORNEY/AGENT INFORMATION:

NAME: Gubinsky, Louis
REGISTRATION NUMBER: 24,835
REFERENCE/DOCKET NUMBER: Q40439

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202)293-7060
TELEFAX: (202)293-7860

INFORMATION FOR SEQ ID NO: 11:

SEQUENCE CHARACTERISTICS:

LENGTH: 237 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 11:

US-10-608-536-11

Query Match 100 %; Score 62; DB 15; Length 237;
Best Local Similarity 100.0%; Pred. No. 0.0052; Mismatches 0;
Matches 12; Conservative 0; Indels 0; Gaps 0;

OY 1 GIEALPRTHESQ 12
Db 182 GIEALPRTHESQ 193

RESULT 4
US-10-663-749-11
Sequence 11, Application US/10663749
Publication No. US20040049015A1
GENERAL INFORMATION:
APPLICANT: TANABE, Tadashi
APPLICANT: YOKOYAMA, CHIEKO
TITLE OF INVENTION: ANTIBODIES SPECIFIC TO HUMAN PROSTACYCLIN SYNTHASE
FILE REFERENCE: Q76409

CURRENT APPLICATION NUMBER: US/10/663, 749
CURRENT FILING DATE: 2003-09-17
PRIOR APPLICATION NUMBER: 09/670, 582
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: 09/037, 758
PRIOR FILING DATE: 1998-01-10
PRIOR APPLICATION NUMBER: 08/578, 706
PRIOR FILING DATE: 1995-12-28
NUMBER OF SEQ ID NOS: 20

RESULT 5
US-10-236-031B-34
Sequence 34, Application US/10236031B
Publication No. US20030219760A1
GENERAL INFORMATION:
APPLICANT: Gordon, Gavin J.
APPLICANT: Jensen, Roderick V.
APPLICANT: Guillans, Steven R.
APPLICANT: Bueno, Raphael
TITLE OF INVENTION: Diagnostic and Prognostic Tests
FILE REFERENCE: B0801/70265 (JRV/JAV)
CURRENT APPLICATION NUMBER: US/10/236, 031B
CURRENT FILING DATE: 2002-09-05
PRIOR APPLICATION NUMBER: US 60/317, 389
PRIOR FILING DATE: 2001-09-05
PRIOR APPLICATION NUMBER: US 60/407, 431
PRIOR FILING DATE: 2002-08-30
NUMBER OF SEQ ID NOS: 102
SOFTWARE: PatentIn version 3.1
SEQ ID NO: 34
LENGTH: 500
TYPE: PRT
ORGANISM: Homo sapiens

US-10-236-031B-34

Query Match 100.0%; Score 62; DB 15; Length 500;
Best Local Similarity 100.0%; Pred. No. 0.012; Mismatches 0;
Matches 12; Conservative 0; Indels 0; Gaps 0;

OY 1 GIEALPRTHESQ 12
Db 182 GIEALPRTHESQ 193

RESULT 6
US-10-608-536-15
Sequence 15, Application US/10608536
Publication No. US20040049015A1
GENERAL INFORMATION:
APPLICANT: TANABE, Tadashi
TITLE OF INVENTION: PROSTACYCLIN SYNTHASE DERIVED FROM HUMAN
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: SUGIRUE, MION, ZINN, MACPEAK & SEAS
STREET: 2100 Pennsylvania Avenue, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20037

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/608, 536
FILING DATE: 30-Jun-2003

CLASSIFICATION: 435
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US/08-578,709
 FILING DATE: 28-DEC-1995
 APPLICATION NUMBER: PCT/JP95/00838
 FILING DATE: 27-APR-1995
 APPLICATION NUMBER: JP 114316/1994
 FILING DATE: 28-APR-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: Gubinsky, Louis
 REGISTRATION NUMBER: 24,835
 REFERENCE/DOCKET NUMBER: Q40439
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202)293-7860
 TELFAX: (202)293-7860
 INFORMATION FOR SEQ ID NO: 15:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 500 amino acids
 TYPE: amino acid
 MOLECULE TOPLOGY: linear
 SEQUENCE DESCRIPTION: SEQ ID NO: 15:
 US-10-608-536-15

Query Match 100.0%; Score 62; DB 15; Length 500;
 Best Local Similarity 100.0%; Pred. No. 0.012; Mismatches 0; Indels 0; Gaps 0;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GIEALPRTHESQ 12
 Db 182 GIEALPRTHESQ 193

RESULT 7
 US-10-663-749-15
 Publication No. US20040092722A1
 Sequence 15, Application US/10663749
 GENERAL INFORMATION:
 APPLICANT: TANABE, TADASHI
 APPLICANT: YOKOYAMA, CHIEKO
 TITLE OF INVENTION: ANTIBODIES SPECIFIC TO HUMAN PROSTACYCLIN SYNTHASE
 FILE REFERENCE: 076409
 CURRENT APPLICATION NUMBER: US/10/663,749
 CURRENT FILING DATE: 2003-09-17
 PRIORITY FILING DATE: 2003-09-17
 PRIORITY APPLICATION NUMBER: 09/670,582
 PRIOR FILING DATE: 2000-09-27
 PRIORITY APPLICATION NUMBER: 09/037,758
 CURRENT APPLICATION NUMBER: US10/663,749
 CURRENT FILING DATE: 2003-09-17
 PRIORITY FILING DATE: 1998-01-10
 PRIORITY APPLICATION NUMBER: 08/578,706
 PRIORITY FILING DATE: 1995-12-28
 NUMBER OF SEQ ID NOS: 20
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 19
 LENGTH: 12
 TYPE: PRT
 PRIORITY APPLICATION NUMBER: 08/578,706
 PRIORITY FILING DATE: 1995-12-28
 NUMBER OF SEQ ID NOS: 20
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 15
 LENGTH: 500
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-663-749-15

Query Match 100.0%; Score 62; DB 15; Length 500;
 Best Local Similarity 100.0%; Pred. No. 0.012; Mismatches 0; Indels 0; Gaps 0;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GIEALPRTHESQ 12
 Db 182 GIEALPRTHESQ 193

RESULT 8
 US-10-923-348-2
 Sequence 2, Application US/10923348
 Publication No. US20050080140A1
 GENERAL INFORMATION:
 APPLICANT: Hatae, Toshihisa

Query Match 100.0%; Score 62; DB 15; Length 500;
 Best Local Similarity 100.0%; Pred. No. 0.012; Mismatches 0; Indels 0; Gaps 0;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GIEALPRTHESQ 12
 Db 182 GIEALPRTHESQ 193

RESULT 9
 US-10-663-749-19
 Sequence 19, Application US/10663749
 Publication No. US20040092722A1
 GENERAL INFORMATION:
 APPLICANT: TANABE, TADASHI
 APPLICANT: YOKOYAMA, CHIEKO
 TITLE OF INVENTION: ANTIBODIES SPECIFIC TO HUMAN PROSTACYCLIN SYNTHASE
 FILE REFERENCE: 076409
 CURRENT APPLICATION NUMBER: US/10/663,749
 CURRENT FILING DATE: 2003-09-17
 PRIORITY FILING DATE: 2000-09-27
 PRIORITY APPLICATION NUMBER: 09/670,582
 PRIOR FILING DATE: 1998-01-10
 PRIORITY APPLICATION NUMBER: 08/578,706
 PRIORITY FILING DATE: 1995-12-28
 NUMBER OF SEQ ID NOS: 20
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 19
 LENGTH: 12
 TYPE: PRT
 ORGANISM: Bos sp.
 US-10-663-749-19

Query Match 66.1%; Score 41; DB 15; Length 12;
 Best Local Similarity 66.7%; Pred. No. 1.4;
 Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 GIEALPRTHESQ 12
 Db 1 GVEARPHTESQ 12

RESULT 10
 US-10-425-115-274140
 Sequence 274140, Application US/10425115
 Publication No. US20040214272A1
 GENERAL INFORMATION:
 APPLICANT: La Rosa, Thomas J.
 APPLICANT: Kovalic, David K.
 APPLICANT: Zhou, Yihua
 APPLICANT: Cao, Yongwei
 TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
 FILE REFERENCE: 38-21(5322,B
 CURRENT APPLICATION NUMBER: US/10/425,115

```

; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 274140
; LENGTH: 360
; TYPE: PRT
; ORGANISM: Zea mays
; OTHER INFORMATION: Clone ID: MRT4577_181603C.1.pep
US-10-425-115-274140

Query Match 64.5%; Score 40; DB 16; Length 360;
Best Local Similarity 77.8%; Pred. No. 81; Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Qy 1 GIEALPRTH 9
Db 272 GIEAIPKTH 280

RESULT 11
US-10-730-930-6590
; Sequence 6590, Application US/10739930
; Publication No. US20040216190A1

; GENERAL INFORMATION:
; APPLICANT: Kovacic, David K.
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH PLANTS AND USES THEREOF FOR PLANT IMPROVEMENT
; TITLE OF INVENTION: PLANTS AND USES THEREOF FOR PLANT IMPROVEMENT
; FILE REFERENCE: 38-21(5327)B
; CURRENT APPLICATION NUMBER: US/10/730, 930
; CURRENT FILING DATE: 2003-12-18
; NUMBER OF SEQ ID NOS: 11088
; SEQ ID NO 6590
; LENGTH: 924
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; FEATURE: OTHER INFORMATION: Clone ID: ARATH-23APR03-C5208_1.p
US-10-730-930-6590

Query Match 64.5%; Score 40; DB 16; Length 924;
Best Local Similarity 60.0%; Pred. No. 2.2e-02; Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
Qy 1 GIEALPRTH 10
Db 118 GIEALPOTHQ 127

RESULT 12
US-10-424-599-269929
; Sequence 269929, Application US/10424599
; Publication No. US2004031072A1

; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovacic, David K.
; APPLICANT: Zhou Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(5322)B
; CURRENT APPLICATION NUMBER: US/10/424, 599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 342271
; LENGTH: 161
; TYPE: PRT
; ORGANISM: Zea mayB
; FEATURE: NAME/KEY: unsure
; LOCATION: (1)..(161)
; OTHER INFORMATION: unsure at all Xaa locations
; OTHER INFORMATION: Clone ID: MRT4577_75314C.1.pep
US-10-424-599-269929

Query Match 61.3%; Score 38; DB 15; Length 61;
Best Local Similarity 100.0%; Pred. No. 28; Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
Qy 1 GIEALPRTHSQ 12
Db 113 GIDALIPRSSEIQ 124

```

RESULT 15
 US-10-425-115-286760
 Sequence 286760, Application US/10425115
 Publication No. US20040214272A1
 ; GENERAL INFORMATION:
 ; APPLICANT: La Rosa, Thomas J.
 ; APPLICANT: Kovalic, David K.
 ; APPLICANT: Zhou, Yihua
 ; APPLICANT: Cao, Yongwei
 ; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
 ; TITLE OF INVENTION: Plants
 ; FILE REFERENCE: 38-21(5322)B
 ; CURRENT APPLICATION NUMBER: US/10/425, 115
 ; CURRENT FILING DATE: 2003-04-28
 ; NUMBER OF SEQ ID NOS: 369326
 ; SEQ ID NO 286760
 ; LENGTH: 179
 ; TYPE: PRT
 ; ORGANISM: Zea mays
 ; FEATURE:
 ; OTHER INFORMATION: Clone ID: MRT4577_2461C.1.pep
 US-10-425-115-286760

RESULT 16
 Query Match 61.3%; Score 38; DB 16; Length 179;
 Best Local Similarity 60.0%; Pred. No. 89;
 Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
 Qy 2 GIEALPRTHES 11 .
 Db 93 LEAIPRSHNS 102

RESULT 17
 US-10-216-774-2168
 ; sequence 2168, Application US/10276774
 ; Publication No. US20040053245A1
 ; GENERAL INFORMATION:
 ; APPLICANT: HYSEQ, Inc.
 ; APPLICANT: Tang, Y., Tom et al
 ; APPLICANT: Prior, Daniel
 ; APPLICANT: Wang, Zhiwei
 ; APPLICANT: Yang, Yonghong
 ; APPLICANT: Ma, Yungqing
 ; APPLICANT: Weng, Gezhi
 ; APPLICANT: Dunn-Coleman, Nigel
 ; APPLICANT: Ward, Michael
 ; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
 ; FILE REFERENCE: 2172-030
 ; CURRENT APPLICATION NUMBER: US/10/216, 774
 ; CURRENT FILING DATE: 2003-11-18
 ; PRIOR APPLICATION NUMBER: 09/560, 875
 ; PRIOR FILING DATE: 2000-04-27
 ; PRIOR APPLICATION NUMBER: 09/496, 914
 ; PRIOR FILING DATE: 2000-02-03
 ; NUMBER OF SEQ ID NOS: 2700
 ; SOFTWARE: Custom
 ; SEQ ID NO 2168
 ; LENGTH: 509
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-216-774-2168

Query Match 61.3%; Score 38; DB 15; Length 509;
 Best Local Similarity 50.0%; Pred. No. 2.7e+02;
 Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
 Qy 1 GIEALPRTHE 10 .
 Db 390 GvQGIPRVHE 399

RESULT 18
 US-10-425-115-269133
 ; sequence 269133, Application US/10425115
 ; Publication No. US20040214272A1
 ; GENERAL INFORMATION:
 ; APPLICANT: La Rosa, Thomas J.
 ; APPLICANT: Kovalic, David K.
 ; APPLICANT: Zhou, Yihua
 ; APPLICANT: Cao, Yongwei
 ; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
 ; FILE REFERENCE: 38-21(5322)B
 ; CURRENT APPLICATION NUMBER: US/10/425, 115
 ; CURRENT FILING DATE: 2003-04-28
 ; NUMBER OF SEQ ID NOS: 369326
 ; SEQ ID NO 269133
 ; LENGTH: 69
 ; TYPE: PRT
 ; ORGANISM: Zea mays
 ; FEATURE:
 ; OTHER INFORMATION: Clone ID: MRT4577_177047C.1.pep
 US-10-425-115-269133

Query Match 59.7%; Score 37; DB 16; Length 69;
 Best Local Similarity 54.5%; Pred. No. 49;
 Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
 Qy 1 GIEALPRTHES 11 .
 Db 50 GFKGFPRTKHS 60

RESULT 19
 US-10-243-552-573
 ; sequence 553, Application US/102435552
 ; Publication No. US20030224379A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Tang, Y., Tom
 ; APPLICANT: Yang, Yonghong
 ; APPLICANT: Wang, Zhiwei
 ; APPLICANT: Ma, Yungqing
 ; APPLICANT: Weng, Gezhi
 ; APPLICANT: Dunn-Coleman, Nigel
 ; APPLICANT: Ward, Michael
 ; TITLE OF INVENTION: Novel Nucleic Acids and
 ; TITLE OF INVENTION: Polypeptides
 ; FILE REFERENCE: 807A
 ; CURRENT APPLICATION NUMBER: US/10/243, 552
 ; CURRENT FILING DATE: 2002-09-12
 ; PRIOR APPLICATION NUMBER: US 60/322, 511
 ; PRIOR FILING DATE: 2001-09-13
 ; PRIOR APPLICATION NUMBER: PCT/US00/35017
 ; PRIOR FILING DATE: 2000-12-22

RESULT 17
 US-10-301-015-2
 Sequence 2, Application US/10301015
 ; Publication No. US20040102619A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Dunn-Coleman, Nigel
 ; APPLICANT: Ward, Michael

```

; PRIOR APPLICATION NUMBER: US 09/488,725
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: PCT/US01/02623
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: US 09/491,404
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: PCT/IS01/03800
; PRIOR FILING DATE: 2001-02-05
; PRIOR APPLICATION NUMBER: US 09/496,914
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: US 09/560,875
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: PCT/US01/04927
; PRIOR FILING DATE: 2001-02-26
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 998
; SOFTWARE: pt_FL_genes Version 5.0
; SEQ ID NO 573
; LENGTH: 410
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-243-552-573

RESULT 20
Query Match      59.7%; Score 37; DB 15; Length 410;
Best Local Similarity 60.0%; Pred. No. 3.3e+02; Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
Oy                2 |EALPRTHES 11
Db                140 LSAIPLRSHEA 149

; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Ross, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(5322)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 191562
; LENGTH: 105
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(105)
; OTHER INFORMATION: unsure at all xaa locations
; OTHER INFORMATION: Clone ID: MRT4577_106284C.1.pep
; US-10-425-115-191562

Query Match      58.1%; Score 36; DB 16; Length 105;
Best Local Similarity 58.3%; Pred. No. 1.2e+02; Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
Oy                1 GIEALPRTTHESQ 12
Db                52 GMETLAPSHESQ 63

; Publication No. US20040005579A1
; GENERAL INFORMATION:
; APPLICANT: Biess et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PA113P1
; CURRENT APPLICATION NUMBER: US10/264,049
; CURRENT FILING DATE: 2003-10-04
; PRIOR APPLICATION NUMBER: PCT/US01/18569
; PRIOR FILING DATE: 2001-06-07
; PRIOR APPLICATION NUMBER: US 60/209,467
; PRIOR FILING DATE: 2000-06-07
; NUMBER OF SEQ ID NOS: 4360
; SOFTWARE: PatentIn Ver. 3.1
; SEQ ID NO 2676
; LENGTH: 126
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-264-049-2676

Query Match      58.1%; Score 36; DB 15; Length 101;
Best Local Similarity 54.5%; Pred. No. 1.1e+02; Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
Oy                1 GIEALPRTTHES 11
Db                2 GVLFLFKTHQS 12

; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Screen, Steven E.
; APPLICANT: Kovalic, David K.

RESULT 21
Query Match      58.1%; Score 36; DB 15; Length 126;
Best Local Similarity 41.7%; Pred. No. 1.4e+02; Matches 5; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
Oy                1 GIEALPRTTHESQ 12
Db                102 GPVSPIPQTHSQ 113

; Publication No. US10425114-68790
; Sequence 68790, Application US/10425114
; LENGTH: 126
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_14456C.1.pep
; US-10-437-963-110387

Query Match      58.1%; Score 36; DB 16; Length 101;
Best Local Similarity 54.5%; Pred. No. 1.1e+02; Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
Oy                1 GIEALPRTTHES 11
Db                2 GVLFLFKTHQS 12

; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Screen, Steven E.
; APPLICANT: Kovalic, David K.

RESULT 22
Query Match      58.1%; Score 36; DB 16; Length 105;
Best Local Similarity 58.3%; Pred. No. 1.2e+02; Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
Oy                1 GIEALPRTTHESQ 12
Db                52 GMETLAPSHESQ 63

; Publication No. US20040005579A1
; GENERAL INFORMATION:
; APPLICANT: Biess et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PA113P1
; CURRENT APPLICATION NUMBER: US10/264,049
; CURRENT FILING DATE: 2003-10-04
; PRIOR APPLICATION NUMBER: PCT/US01/18569
; PRIOR FILING DATE: 2001-06-07
; PRIOR APPLICATION NUMBER: US 60/209,467
; PRIOR FILING DATE: 2000-06-07
; NUMBER OF SEQ ID NOS: 4360
; SOFTWARE: PatentIn Ver. 3.1
; SEQ ID NO 2676
; LENGTH: 126
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-264-049-2676

Query Match      58.1%; Score 36; DB 15; Length 126;
Best Local Similarity 41.7%; Pred. No. 1.4e+02; Matches 5; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
Oy                1 GIEALPRTTHESQ 12
Db                102 GPVSPIPQTHSQ 113

; Publication No. US10425114-68790
; Sequence 68790, Application US/10425114
; LENGTH: 126
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_14456C.1.pep
; US-10-437-963-110387

```

APPLICANT: Tabaska, Jack E
 APPLICANT: Cao, Yongwei
 TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With Title of Invention: Plants and Uses Thereof for Plant Improvement
 FILE REFERENCE: 38-21(53313)B
 CURRENT FILING DATE: 2003-04-28
 NUMBER OF SEQ ID NOS: 73128
 SEQ ID NO: 68790
 LENGTH: 141
 TYPE: PRT
 ORGANISM: Zea mays
 FEATURE:
 OTHER INFORMATION: Clone ID: UCC-ZMFLM017018C01_FLI.pep
 US-10-425-114-68790

Query Match Similarity 58.1%; Score 36; DB 15; Length 141;
 Best Local Similarity 87.5%; Pred. No. 1.6e+02;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 5 LPRTHESQ 12
 Db 1 LPPTHESQ 8

RESULT 24
 US-10-425-115-303972
 Sequence 303972, Application US/10425115
 Publication No. US20040214272A1
 GENERAL INFORMATION:
 APPLICANT: La Rosa, Thomas J.
 APPLICANT: Kovacic, David K.
 APPLICANT: Zhou, Yihua
 APPLICANT: Cao, Yongwei
 TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With Title of Invention: Plants
 FILE REFERENCE: 38-21(5322)B
 CURRENT APPLICATION NUMBER: US/10/425,115
 CURRENT FILING DATE: 2003-04-28
 NUMBER OF SEQ ID NOS: 369326
 SEQ ID NO: 303972
 LENGTH: 150
 TYPE: PRT
 ORGANISM: Zea mays
 FEATURE:
 NAME/KEY: unsure
 LOCATION: (1)..(150)
 OTHER INFORMATION: unsure at all xaa locations
 FEATURE:
 OTHER INFORMATION: Clone ID: MRT4577_40293C.1.pep
 US-10-425-115-303972

Query Match Similarity 58.1%; Score 36; DB 16; Length 150;
 Best Local Similarity 87.0%; Pred. No. 1.7e+02;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 2 IEALPRTH 9
 Db 105 VEALPRVH 112

RESULT 25
 US-10-282-122A-49712
 Sequence 49712, Application US/10282122A
 Publication No. US20040214272A1
 GENERAL INFORMATION:
 APPLICANT: Wang, Liangsu
 APPLICANT: Zamudio, Carlos
 APPLICANT: Malone, Cheryl
 APPLICANT: Hanelbeck, Robert
 APPLICANT: Ohlson, Karl
 APPLICANT: Zyskind, Judith
 APPLICANT: Wall, Daniel

Query Match Similarity 58.1%; Score 36; DB 16; Length 398;
 Best Local Similarity 54.5%; Pred. No. 4.8e+02;
 Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
 QY 2 IEALPRTHSQ 12
 Db : : |||||

RESULT 26
 US-10-739-930-7940
 Sequence 7940, Application US/10739930
 Publication No. US20040216190A1
 GENERAL INFORMATION:
 APPLICANT: Kovacic, David K.
 TITLE OF INVENTION: NUCLEAR ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH TITLE OF INVENTION: PLANTS AND USES THEREOF FOR PLANT IMPROVEMENT
 FILE REFERENCE: 38-21(5337)B
 CURRENT APPLICATION NUMBER: US/10/739,930
 CURRENT FILING DATE: 2003-12-18
 NUMBER OF SEQ ID NOS: 11088
 SEQ ID NO: 7940
 LENGTH: 398
 TYPE: PRT
 ORGANISM: Zea mays
 FEATURE:
 OTHER INFORMATION: Clone ID: ZEAMA-23NPR03-C32089_2.p
 US-10-739-930-7940

Query Match Similarity 58.1%; Score 36; DB 16; Length 398;
 Best Local Similarity 54.5%; Pred. No. 4.8e+02;
 Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
 QY 2 IEALPRTHSQ 12
 Db : : |||||

Db 51 VASFPRTPHSQ 61

RESULT 27

US-10-369-493-11658

; Sequence 11658, Application US/10369493

; Publication No. US20030233675A1

GENERAL INFORMATION:

APPLICANT: Cao, Yongwei

APPLICANT: Hinkle, Gregory J.

APPLICANT: Slater, Steven C.

APPLICANT: Goldman, Barry S.

APPLICANT: Chen, Xianfeng

TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF

TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES

FILE REFERENCE: 38-10(52052)B

CURRENT APPLICATION NUMBER: US/10/369, 493

CURRENT FILING DATE: 2003-02-28

PRIORITY NUMBER: US 60/360, 039

Query Match 58.1%; Score 36; DB 15; Length 403;

Best Local Similarity 70.0%; Pred. No. 4.9e+02; Mismatches 0; Indels 0; Gaps 0;

Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 IEALPRTHES 11

Db 130 ITGLPRNHEs 139

RESULT 28

US-10-669-493-14548

; Sequence 14548, Application US/10369493

; Publication No. US20030233675A1

GENERAL INFORMATION:

APPLICANT: Cao, Yongwei

APPLICANT: Hinkle, Gregory J.

APPLICANT: Slater, Steven C.

APPLICANT: Goldman, Barry S.

APPLICANT: Chen, Xianfeng

TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF

TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES

FILE REFERENCE: 38-10(52052)B

CURRENT APPLICATION NUMBER: US/10/369, 493

CURRENT FILING DATE: 2003-02-28

PRIORITY NUMBER: US 60/360, 039

PRIORITY NUMBER: US 60/360, 039

NUMBER OF SEQ ID NOS: 47374

SEQ ID NO 14548

LENGTH: 403

TYPE: PRT

ORGANISM: Agrobacterium tumefaciens

US-10-369-493-11658

Query Match 58.1%; Score 36; DB 15; Length 403;

Best Local Similarity 70.0%; Pred. No. 4.9e+02; Mismatches 0; Indels 0; Gaps 0;

Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 IEALPRTHES 11

Db 130 ITGLPRNHEs 139

RESULT 29

US-10-369-493-15116

; Sequence 15116, Application US/10369493

; Publication No. US20030233675A1

Query Match 58.1%; Score 36; DB 15; Length 403;

Best Local Similarity 70.0%; Pred. No. 4.9e+02; Mismatches 0; Indels 0; Gaps 0;

Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 IEALPRTHES 11

Db 130 ITGLPRNHEs 139

Search completed: August 1, 2005, 09:01:52

Job time : 157 secs

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